

Scoring table:	BLOSUM62	ALIGNMENTS				
Gapop:	10.0	Gapext: 0.5				
Searched:	1612378 seqs, 512079187 residues					
Total number of hits satisfying chosen parameters:	1612378					
Minimum DB seq length:	0					
Maximum DB seq length:	2000000000					
Post-processing:	Minimum Match 0% Maximum Match 100%					
	Listing first 45 summaries					
Database :	UniProt_03_*					
	1: uniprot_sprot: 2: uniprot_trembl: *					
Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.					
SUMMARIES						
Result No.	Score	Query	Match	Length	DB ID	Description
1	2042	100.0	394	1	CIW3_HUMAN	014649 homo sapien
2	1850.5	90.6	411	1	CIW3_RAT	054912 rattus norvegicus
3	1840.5	90.1	409	1	CIW3_MOUSE	035111 mus musculus
4	1333	84.8	392	2	Q9ESN5	098655 rattus norvegicus
5	1298.5	65.3	299	2	Q90X34	096034 mus musculus
6	1298.5	63.6	301	2	Q9ESM4	Q9esm4 rattus norvegicus
7	1150	56.3	374	2	Q63Z10	Q63z10 xenopus laevis
8	1116	54.7	374	1	CIW9_HUMAN	Q9pc2 homo sapien
9	1069.5	52.4	365	1	CIW9_CAVPO	Q9j158 cavia porcellus
10	999	48.9	396	2	Q922V6	Q9j3v6 rattus norvegicus
11	960.5	47.0	395	2	Q9JJD4	Q911d4 rattus norvegicus
12	924	45.2	237	1	CIW9_RAT	Q98908 rattus norvegicus
13	916.5	44.9	318	1	CIWF_RAT	Q8510 rattus norvegicus
14	846	41.4	330	1	CIWF_HUMAN	Q9h427 homo sapien
15	820	40.2	329	2	Q171S5	Q171s5 cenorhabditis elegans
16	777	38.1	340	2	Q9VBH0	Q9vbh0 drosophila melanogaster
17	769	37.7	307	2	Q7PZH9	Q7ph9 anopheles gambiae
18	760.5	37.2	345	2	Q7QG51	Q7qg51 anopheles gambiae
19	742	36.3	398	2	Q9VPFS9	Q9vpfs9 drosophila melanogaster
20	732.5	35.9	270	2	Q9JU57	Q9ju57 cavia porcellus
21	599	29.3	364	2	Q7E790	Q7e790 cenorhabditis elegans
22	58.5	27.4	121	2	Q86T3	Q86t3 orcyctolagus cuniculus
23	373	18.3	405	1	CIWD_MOUSE	Q9ri55 mus musculus
24	370	18.1	411	1	CIW2_MOUSE	P91438 mus musculus
25	369	18.1	405	1	CIWD RAT	Q9arbo rattus norvegicus
26	367	18.0	426	2	Q920B6	Q920b6 rattus norvegicus
27	366	17.9	414	2	Q6PP9	Q96p9 mus musculus
28	364	17.8	426	1	CIW2_HUMAN	Q95069 homo sapiens
29	363	17.8	411	2	Q9NRT2	Q9nrt2 homo sapiens
30	361	17.7	309	1	CING_HUMAN	Q96755 homo sapiens
31	360	17.6	411	2	Q8HY88	Q8hy88 bos taurus

Scoring table:	BLOSUM62	ALIGNMENTS
Gapop:	10.0	Gapext: 0.5
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Total number of hits satisfying chosen parameters:	1612378	
Minimum DB seq length:	0	
Maximum DB seq length:	2000000000	
Post-processing:	Minimum Match 0% Maximum Match 100%	
	Listing first 45 summaries	
Database :	UniProt_03_*	
	1: uniprot_sprot: 2: uniprot_trembl: *	
Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	
RESULT 1		
CTW3_HUMAN	STANDARD;	PRT; 394 AA.
ID	014649;	
AC		
DT	16-OCT-2001 (Rel. 40, Created)	
DT	16-OCT-2001 (Rel. 40, Last sequence update)	
DT	05-JUL-2004 (Rel. 44, Last annotation update)	
DE	Potassium channel subfamily K member 3 (Acid-sensitive potassium channel protein TASK-1) (TWIK-related acid-sensitive K+ channel 1)	
DE	(Two pore potassium channel KTC-1).	
GN	Name=KCNK3; Synonyms=TASK, TASK1;	
OS	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OC		
OX		
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE-Kidney;	
RC	MEDLINE=97459932; PubMed=9312005; DOI=10.1093/emboj/16.17.5464;	
RA	Duprat F., Lescage P., Fink M., Reyes R., Heurteaux C., Lazdunski M.; "TASK, a human background K <sup>+</sup> channel to sense external pH variations near physiological pH,"	
RT	EMBO J. 16:5464-5471(1997).	
BL		
RN		
RP	SEQUENCE FROM N.A.	
RC	TISSUE-Heart;	
RC	Lopes C.M.B., Gallagher P.G., Buck M.E., Butler M.H., Goldstein S.A.N.; "Proton block and voltage-gating are potassium-dependent in the cardiac leak channel Kcnk3.";	
RA	RT "Proton block and voltage-gating are potassium-dependent in the cardiac leak channel Kcnk3.";	
RA	Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.	
RL		
RN		
RP	ACTIVATION	
RX	MEDLINE=99254548; PubMed=10321245; DOI=10.1038/8084;	
RA	Patel A.J., Honore E., Leage E.P., Fink M., Romeo G., Lazdunski M.; "Inhalational anesthetics activate two-pore-domain background K <sup>+</sup> channels."	
RT	RT "Inhalational anesthetics activate two-pore-domain background K <sup>+</sup> channels."	
BL	RT Nat. Neurosci. 2:422-426(1999).	
RN		
RP	MUTAGENESIS OF HIS-98.	
RX	MEDLINE=21335313; PubMed=11680614;	
RA	Ashmore I., Goodwin P.A., Stanfile P.R.; "TASK-5, a novel member of the tandem pore K <sup>+</sup> channel family.";	
RT	RT "TASK-5, a proton block and voltage-gating are potassium-dependent in the membrane. Acts as an outward rectifier when external potassium concentration is low. When external potassium concentration is high, current is inward.	
RL	RT Pfleugers Arch. 442:828-833(2001).	
CC	-1- FUNCTION: pH-dependent, voltage-insensitive, background potassium channel protein. Rectification direction results from potassium ion concentration on either side of the membrane. Acts as an outward rectifier when external potassium concentration is low.	
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).	
CC	-1- TISSUE SPECIFICITY: Widespread expression in adult. Strongest expression in pancreas and placenta. Lower expression in brain, lung, prostate, heart, kidney, uterus, small intestine and colon.	
CC	-1- MISCELLANEOUS: Inhibited by external acidification. Activated by	

halothane and isoflurane.  
 CC - SIMILARITY: Belongs to the two pore domain potassium channel  
 (TC 1.A.1.B) family.

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CC EMBL; AF006523; AAC5177\_1; -;  
 DR GenBank; HGNC:6278; KCMK3.  
 DR MIM: 603220; -;  
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
 DR GO; GO:0005267; F:potassium channel activity; TAS.  
 DR GO; GO:0006613; F:potassium ion transport; TAS.  
 DR GO; GO:000268; F:synaptic transmission; TAS.  
 DR InterPro; IPR005821; Ion trans.  
 DR InterPro; IPR003280; K+channel\_2pore.  
 DR InterPro; IPR001622; K+channel\_pore.  
 DR InterPro; IPR004406; TASK1\_channel.  
 DR InterPro; IPR003092; TASK\_2\_channel.  
 DR PRINTS; PR01333; Ion trans\_1.  
 DR PRINTS; PR01584; 2POREKCHANNEL.  
 DR PRINTS; PR01095; TASKCHANNEL.  
 KW Glycoprotein; Ion transport; Ionic channel; Potassium; Potassium channel; Transmembrane; Transport; Voltage-gated channel.  
 KW Potassium channel; Transmembrane; Transport; Voltage-gated channel.  
 FT DOMAIN 1 8  
 FT TRANSMEM 9 29  
 FT DOMAIN 78 101  
 FT TRANSMEM 108 128  
 FT DOMAIN 129 158  
 FT TRANSMEM 159 179  
 FT DOMAIN 184 207  
 FT TRANSMEM 223 243  
 FT DOMAIN 244 394  
 FT CARBOHYD 53 53  
 FT MUTAGEN 98 98  
 SQ SEQUENCE 394 AA; 43518 MW; 9FP4C8266FG15FB7 CRC64;

Query Match 100.0%: Score 2042; DB 1; Length 394;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-153; Indels 0; Gaps 0;  
 Matches 394; Conservative 0; Mismatches 0;

1 MKRQNYRTIALIVCTFVYLLGAAVEDALESSPELIERQRLERQOERARYNLSCQGYE 60  
 1 MKRQNYRTIALIVCTFVYLLGAAVEDALESSPELIERQRLERQOERARYNLSCQGYE 60

Db 61 ELERVVLLPKPHAGVQRFASSPFYATITVITIGKHAAPSTDGKVKFCMFYALLGPL 120  
 61 ELERVVLLPKPHAGVQRFASSPFYATITVITIGKHAAPSTDGKVKFCMFYALLGPL 120

Qy 121 TLWFOSEIGERINTLVRYLLHRAKKGLICMRADVSMANVLFIGFFSCISTLGAAAFSH 180  
 1 MKRQNYRTIALIVCTFVYLLGAAVEDALESSPELIERQRLERQOERARYNLSCQGYE 60

Db 121 TLWFOSEIGERINTLVRYLLHRAKKGLICMRADVSMANVLFIGFFSCISTLGAAAFSH 180

Qy 181 YEHWTFFPQAYYCFITLTIGFDDYVALQKDQALQTQPYQYAFSFWYLTLGTIVGAFLN 240  
 1 MKRQNYRTIALIVCTFVYLLGAAVEDALESSPELIERQRLERQOERARYNLSCQGYE 60

Db 181 YEHWTFFPQAYYCFITLTIGFDDYVALQKDQALQTQPYQYAFSFWYLTLGTIVGAFLN 240

Qy 241 LVVLRFMVMNAEDEKRDEHLRAALTRNGQAGGGGGSSAHTDTASSTAAGGGGRNVI 300  
 241 LVVLRFMVMNAEDEKRDEHLRAALTRNGQAGGGGGSSAHTDTASSTAAGGGGFNNVY 300

Db 301 AEVHFQSMCSCWYKSEKBLQYSIPMIIPRDLSSTDTCVEOSHSSPGGGYSDTFSRR 360  
 301 AEVHFQSMCSCWYKSEKBLQYSIPMIIPRDLSSTDTCVEOSHSSPGGGYSDTFSRR 360

Qy 361 CLCGGAPRSAISSVSTGLHSLSFRGLMKRRSSV 394

Db 361 CLCGGAPRSAISSVSTGLHSLSFRGLMKRRSSV 394

RESULT 2  
 CIW3\_RAT STANDARD; PRT; 411 AA.  
 ID CIW3\_RAT  
 AC 9912;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 05-JUN-2004 (Rel. 44, Last annotation update)  
 DE Potassium channel K member 3 (Acid-sensitive potassium channel protein TASK1) (TWIK-related acid-sensitive K<sub>+</sub> channel 1).  
 DE (Two pore potassium channel, Kr3.1).  
 DE Name=icnk3; Synonyms=Task; Task1;  
 OS Rattus norvegicus (Rat).  
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Muridae; Murinae; Rattus.  
 NCBI\_TaxID=10116;  
 RN [1]  
 RP SOURCE FROM N.A.  
 RC TISSUE=Cerebellum;  
 RX MBDBLINE=98099797; PubMed=9437008;  
 RA Leonoudakis D., Gray A.T., Winegar B.D., Kindler C.H., Harada M., Taylor D.M., Chavez R.A., Forrayeth J.R., Yost C.S.;  
 RA "An open rectifier potassium channel with two pore domains in tandem cloned from rat cerebellum."  
 RL J. Neurosci. 18:868-877(1998).  
 DR -!  
 DR FUNCTION: pH-dependent, voltage-insensitive, background potassium channel protein. Rectification direction results from potassium ion concentration on either side of the membrane. Acts as an outward rectifier when external potassium concentration is low, current is inward.  
 DR (By similarity),  
 CC -!  
 CC SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -!  
 CC TISSUE SPECIFICITY: Strongest expression in heart. Moderate expression in lung and brain. Low levels in liver, kidney and skeletal muscle.  
 CC -!  
 CC MISCELLANEOUS: Inhibited by extracellular acidification, zinc, bupivacaine and phenytoin. Activated by protein kinase A.  
 CC -!  
 CC SIMILARITY: Belongs to the two pore domain potassium channel (TC 1.A.1.B).  
 CC -!  
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 CC -!  
 CC EMBL; AF006523; AAC5177\_1; -;  
 DR RGD; 61997; Kcnk3.  
 DR InterPro; IPR005821; Ion trans.  
 DR InterPro; IPR003280; K+channel\_2pore.  
 DR InterPro; IPR001622; K+channel\_Pore.  
 DR InterPro; IPR005406; TASK1\_channel.  
 DR InterPro; IPR003092; TASK\_Channel.  
 DR PFam; PF00523; Ion\_trans\_B; 1.  
 DR PRINTS; PRO1333; 2POREKCHANNEL.  
 DR PRINTS; PRO1584; TASK1CHANNEL.  
 DR Glycoprotein; Ion transport; TASKCHANNEL.  
 KW Potassium channel; Transmembrane; Transport; Ionic channel; Potassium; Cytoplasmic (Potential).  
 DR Transmembrane; Transport; Voltage-gated channel.  
 DR InterPro; IPR005821; Ion trans.  
 DR InterPro; IPR003280; K+channel\_2pore.  
 DR InterPro; IPR001622; K+channel\_Pore.  
 DR InterPro; IPR005406; TASK1\_channel.  
 DR InterPro; IPR003092; TASK\_Channel.  
 DR PFam; PF00523; Ion\_trans\_B; 1.  
 DR PRINTS; PRO1333; 2POREKCHANNEL.  
 DR PRINTS; PRO1584; TASK1CHANNEL.  
 DR Glycoprotein; Ion transport; TASKCHANNEL.  
 KW Potassium channel; Transmembrane; Transport; Ionic channel; Potassium; Cytoplasmic (Potential).  
 DR Transmembrane; Transport; Voltage-gated channel.  
 DR InterPro; IPR005821; Ion trans.  
 DR InterPro; IPR003280; K+channel\_2pore.  
 DR InterPro; IPR001622; K+channel\_Pore.  
 DR InterPro; IPR005406; TASK1\_channel.  
 DR InterPro; IPR003092; TASK\_Channel.  
 DR PFam; PF00523; Ion\_trans\_B; 1.  
 DR PRINTS; PRO1333; 2POREKCHANNEL.  
 DR PRINTS; PRO1584; TASK1CHANNEL.  
 DR Glycoprotein; Ion transport; TASKCHANNEL.  
 KW Potassium channel; Transmembrane; Transport; Ionic channel; Potassium; Cytoplasmic (Potential).  
 DR Transmembrane; Transport; Voltage-gated channel.  
 DR InterPro; IPR005821; Ion trans.  
 DR InterPro; IPR003280; K+channel\_2pore.  
 DR InterPro; IPR001622; K+channel\_Pore.  
 DR InterPro; IPR005406; TASK1\_channel.  
 DR InterPro; IPR003092; TASK\_Channel.  
 DR PFam; PF00523; Ion\_trans\_B; 1.  
 DR PRINTS; PRO1333; 2POREKCHANNEL.  
 DR PRINTS; PRO1584; TASK1CHANNEL.  
 DR Glycoprotein; Ion transport; TASKCHANNEL.  
 KW Potassium channel; Transmembrane; Transport; Ionic channel; Potassium; Cytoplasmic (Potential).  
 DR Transmembrane; Transport; Voltage-gated channel.  
 DR InterPro; IPR005821; Ion trans.  
 DR InterPro; IPR003280; K+channel\_2pore.  
 DR InterPro; IPR001622; K+channel\_Pore.  
 DR InterPro; IPR005406; TASK1\_channel.  
 DR InterPro; IPR003092; TASK\_Channel.  
 DR PFam; PF00523; Ion\_trans\_B; 1.  
 DR PRINTS; PRO1333; 2POREKCHANNEL.  
 DR PRINTS; PRO1584; TASK1CHANNEL.  
 DR Glycoprotein; Ion transport; TASKCHANNEL.

FT      CARBOHYD      53      AA;      411 AA;      53      N-linked (GlcNAc- .) (Potential).  
 SQ      SEQUENCE      411 AA;      45276 MW;      D2778016E09B2BFS CRC64;  
 Query Match      90.6%;      Score 180.5;      DB 1;      Length 411;  
 Best Local Similarity      88.3%;      Pred: No. 2e-138;  
 Matches 363;      Conservative 8;      Mismatches 23;      Indels 17;      Gaps 2;  
 QY      1 MKRONVRLALIVCTFTYLVGAADFVALESEPELIERORLERRQELRPARYNLSOGGYE 60  
 DB      1 MKRNVRTLAKPKHAGVQMRPAGSPTYFAITVITIGYHAAPSTDGKVFCMFTALLGPL 60  
 DB      121 TLVNFOSLGERINTLVRLHAKGLGRADYSMANNVLIGFSCSITLIGAASH 180  
 DB      121 TLVNFOSLGERINTFVRLHAKGLGRADYSMANNVLIGFVSCSITLIGAASY 180  
 QY      61 ELERVVLRLKPKHAGVQMRPAGSPTYFAITVITIGYHAAPSTDGKVFCMFTALLGPL 120  
 QY      181 YEHNTFFQAYYYCFITLTIGFDYVALQDOALQTOPOVYAFSFVYLTGTYVIGPLN 240  
 DB      181 YERATFFQAYYYCITLTIGFDYVALQDOALQTOPOVYAFSFVYLTGTYVIGPLN 240  
 QY      241 LVLURFMTNAEDEKDAEHLALTRNGAGGGG-----GGSAHTTDASSTAR- 291  
 DB      241 LVLURFMTNAEDEKDAEHLALTHNGAGGGLSCLSGSLGDGVRPRDPYCAAG 300  
 QY      292 -----GGGGFNRVYAVLHFOSMCSCWYSREKQYSPIMIPDLSTSSTDTCVHS 343  
 DB      301 GMGVGVGVGGSGFNRVYAVLHFOSMCSCWYSREKQYSPIMIPDLSTSSTDTCVHS 360  
 QY      344 HSSPGGGGRYSDTPSRRCLCSGAPRSAISSVSTGLHSLSITFRGMKRSVV 394  
 DB      361 HSSPGGGGRYSDTPSHPCLCSGATORSAISVSTGLHSLSATFRGLMKRSVV 411

RESULT 3  
 C1W3\_MOUSE  
 ID      C1W3\_MOUSE      STANDARD;      PRT;      409 AA.  
 AC      O35163;  
 DT      16-OCT-2001 (Rel. 40, Created)  
 DR      16-OCT-2001 (Rel. 40, Last sequence update)  
 DR      05-JUL-2004 (Rel. 44, Last annotation update)  
 DE      Potassium channel subfamily K member 3 (Acid-sensitive potassium channel protein TASK-1) (TWIK-related acid-sensitive K+ channel 1)  
 DE      (cardiac two-pore background K+ channel) (ctBak-1) (Two pore potassium channel KT3.1).  
 DE      Name=Kcnk3;      Synonyms=Ctcbak, TASK, Task1;  
 OS      Mus musculus (Mouse).  
 OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.  
 OC      [1]  
 RN      10090;  
 RP      SEQUENCE FROM N.A.  
 RC      TISSUE-Heart;  
 RX      MEDLINE:98165556;      PubMed:9506712;  
 RA      Kim D., Fujita A., Horio Y., Kurachi Y.;  
 RR      "Cloning and functional expression of a novel cardiac two-pore background K+ channel (ctBak-1)." ;  
 RL      Circ. Res. 82:513-518 (1998).  
 RN      SEQUENCE FROM N.A.  
 RC      TISSUE-Heart;  
 RX      MEDLINE:20287574;      PubMed:10748056;      DOI=10.1074/jbc.M001948200;  
 RA      Lopes C.M., Gallagher P.G., Buck M.E., Butler M.H., Goldstein S.A. ;  
 RR      "Proton block and voltage gating are potassium-dependent in the cardiac leak channel Kcnk3";  
 RL      J. Biol. Chem. 275:16369-16378 (2000).  
 RN      SEQUENCE FROM N.A.  
 RP      MEDLINE:97455932;      PubMed:9312005;      DOI=10.1093/embj/16.17.5464;  
 RA      Duprat F., Lesage P., Pink M., Reyes R., Heurtault C., Izadnouski M. ;  
 RT      "TASK, a human background K+ channel to sense external pH variations

RT      near physiological pH.";  
 RL      EMBO J. 16:546-547(1997).  
 CC      -I- FUNCTION: pH-dependent, voltage-insensitive, background potassium channel protein. Rectification direction results from potassium ion concentration on either side of the membrane. Acts as an outward rectifier when external potassium concentration is low. When external potassium concentration is high, current is inward (By similarity).  
 CC      -I- SUBUNIT: Homodimer (Potential).  
 CC      -I- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC      -I- TISSUE SPECIFICITY: Very strong expression in heart, also detected in kidney, brain, skin, testis, lung, skeletal muscle, small intestine and stomach. Not detected in liver, thymus or spleen.  
 CC      -I- MISCELLANEOUS: Inactivated by barium.  
 CC      -I- SIMILARITY: Belongs to the two pore domain potassium channel (TC 1.A.8) family.  
 CC      ---  
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 CC      ---  
 DR      AB008537;      BAA2543.1;      -;  
 DR      AF241798;      AAF8141.1;      -;  
 DR      AF245208;      AAF81418.1;      JOINED.  
 DR      AF245208;      AAG2913.1;      -;  
 DR      AF065162;      AAC5336.1;      -;  
 DR      AF006824;      AAC5336.1;      -;  
 DR      AB013345;      BAA2834.9;      -;  
 DR      MGI: MGI:1100509;      Kcnk3.  
 DR      InterPro;      IPRO05821;      Ion trans.  
 DR      InterPro;      IPRO05280;      K+ channel 2 pore.  
 DR      InterPro;      IPRO01622;      K+channel\_pore.  
 DR      InterPro;      IPRO05406;      TASK1\_channel.  
 DR      InterPro;      IPRO03092;      TASK\_ channel.  
 DR      Pfam;      PF00520;      Ion trans; 1.  
 DR      PRINTS;      PRO1333;      2PORISKCHANNEL.  
 DR      PRINTS;      PRO1584;      2PORISKCHANNEL.  
 DR      PRINTS;      PRO1095;      TASKCHANNEL.  
 KW      Glycoprotein;      Ion transport;      Ionic channel;      Potassium;  
 KW      Potassium channel;      Transmembrane;      Transport;      Voltage-gated channel.  
 FT      DOMAIN      1      8  
 FT      TRANSMEM      9      29  
 FT      DOMAIN      78      101  
 FT      TRANSMEM      108      128  
 FT      DOMAIN      129      158  
 FT      TRANSMEM      159      179  
 FT      DOMAIN      184      207  
 FT      TRANSMEM      223      243  
 FT      DOMAIN      244      409  
 FT      CARBOHYD      53      53  
 FT      CONFLICT      4      4  
 FT      CONFLICT      123      123  
 SQ      SEQUENCE      409 AA;      45068 MW;      35238E011AAC5687 CRC64;  
 Query Match      90.1%;      Score 1840.5;      DB 1;      Length 409;  
 Best Local Similarity      88.5%;      Pred: No. 1..3e-137;  
 Matches 362;      Conservative 7;      Mismatches 25;      Indels 15;      Gaps 2;

QY      1 MKRQNYVTALIYVCTTYLYGRAVFDALESEPELIERQRLERLRQELRARYNLSGGXY 60  
 DB      1 MKRQNYVTALIYVCTTYLYGRAVFDALESEPELIERQRLERLRQELRARYNLSGGXY 60  
 QY      61 ELERVVRLRKPHAGVQMRPAGSPTYFAITVITIGYHAAPSTDGKVFCMFTALLGPL 120  
 DB      61 ELERVVRLRKPHAGVQMRPAGSPTYFAITVITIGYHAAPSTDGKVFCMFTALLGPL 120  
 QY      121 TLVNFOSLGERINTVYLLHAKGLGRADYSMANNVLIGFSCSITLIGAASH 180  
 DB      121 TLVNFOSLGERINTVYLLHAKGLGRADYSMANNVLIGFSCSITLIGAASH 180

Qy	181	YEHWTFQQAYYYCPIITLTIGFEDYVALKODALQTOPQYAFSFVYILTLGTLVIGAPLN	240	Db	162	YERWTFFQAYYYCPIITLTIGFEDYVALKODALQTOPQYAFSFVYILTLGTLVIGAPLN	221		
Db	181	YEWTFQQAYYYCPIITLTIGFEDYVALKODALQTOPQYAFSFVYILTLGTLVIGAPLN	240	Qy	241	LVLRLMFTMNAEDEKRDAAEHLTTRNGQAGGGG-----GGSAAHTTDTASSTAA-	291		
Qy	241	LVLRLMFTMNAEDEKRDAAEHLTTRNGQAGGGG-----GGSAAHTTDTASSTAA-	291	Db	221	LVLRLMFTMNAEDEKRDAAEHLTTRNGQAGGLGGJSLCLSGSLGDSVRPRDEVTAAG	281		
Db	241	LVLRLMFTMNAEDEKRDAAEHLTTRNGQAGGGS-----GGSAAHTTDTASSTAA-	300	Qy	292	-----GGGGFRNYYAETLHFQSMCSCLMYKSREKQLOYSIPMILPDLSTSDFTCVEQS	343		
Qy	292	-----GGGGFRNYYAETLHFQSMCSCLMYKSREKQLOYSIPMILPDLSTSDFTCVEQS	345	Db	282	GNGVTVGVSFGFRNYYAETLHFQSMCSCLMYKSREKQLOYSIPMILPDLSTSDFTCVEHS	341		
Db	301	GVGIVGVGCGSGFRNYYAETLHFQSMCSCLMYKSREKQLOYSIPMILPDLSTSDFTCVEHS	360	Qy	344	HSSPGGGGRYSDTPSPRCLCGAPSIAISSVYSTGHLSLTERGLMKRSSV	394		
Qy	346	SPGGRGRYSDTPSPRCLCGAPSIAISSVYSTGHLSLTERGLMKRSSV	394	Db	342	HSSPGGGGRYSDTPSPHCLCGTQSAISSVYSTGHLSLTERGLMKRSSV	392		
Db	361	SPGGGXSYDTSHPCLCGTQSAISSVYSTGHLSLAFGLMKRSSV	409	RESULT 5					
Q9QX34									
ID	Q9QX34	PRELIMINARY;	PRT;	299 AA.	ID	Q9QX34	PRELIMINARY;	PRT;	299 AA.
AC	Q9BSM5	PRELIMINARY;	PRT;	392 AA.	AC	Q9QX34;	PRELIMINARY;	PRT;	299 AA.
DT	01-MAR-2001	(TREMBLrel.	16, Created)		DT	01-MAY-2000	(TREMBLrel.	13, Created)	
DT	01-MAR-2001	(TREMBLrel.	16, Last sequence update)		DT	01-MAY-2000	(TREMBLrel.	13, Last sequence update)	
DT	01-JUN-2003	(TREMBLrel.	24, Last annotation update)		DT	01-JUN-2003	(TREMBLrel.	24, Last annotation update)	
DR	Putative potassium channel DP4 (fragment).						Putative potassium channel DP4 (fragment).		
GN	Name=Kcnk3;				GN	Name=Kcnk3;			
OS	Mus musculus	(Mouse).			OS	Mus musculus	(Mouse).		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
RN	[1] NCBITaxID=10116;				RN	[1] NCBITaxID=10116;			
RP	SEQUENCE FROM N.A.						SEQUENCE FROM N.A.		
RA	Gan L., Joiner W.J., Quinn A.M., Wang L.-Y., Hughes T.,				RA	Gan L., Joiner W.J., Quinn A.M., Wang L.-Y., Hughes T.,			
RL	Kaczmarek L.K.,				RL	Kaczmarek L.K.,			
CC	Submitted (SEP-1997) to the EMBL/GenBank/DDJB databases.				CC	Submitted (SEP-1997) to the EMBL/GenBank/DDJB databases.			
CC	-1 SIMILARITY: Belongs to the two pore domain potassium channel (TC 1.A.1.8) family.				CC	-1 SIMILARITY: Belongs to the two pore domain potassium channel (TC 1.A.1.8) family.			
DR	EMBL; AB04823; BAB16710; 1.				DR	EMBL; AF022821; ADD09338; 1.			
DR	GO; GO:00016021; C:integral to membrane; TAS.				DR	GO; GO:00016021; C:integral to membrane; TAS.			
DR	DR InterPro; IPR005821; Ion transport.				DR	DR InterPro; IPR005821; Ion transport.			
DR	GO; GO:0005216; F:ion channel activity; IEA.				DR	DR InterPro; IPR003280; K+channel_2pore.			
DR	GO; GO:0006811; F:ion transport; IEA.				DR	DR InterPro; IPR001622; K+channel_pore.			
DR	GO; GO:0006813; F:potassium ion transport; IEA.				DR	DR InterPro; IPR005406; TASK1_channel.			
DR	DR InterPro; IPR005221; Ion transport.				DR	DR InterPro; IPR003092; TASK2_channel.			
DR	DR InterPro; IPR003280; K+channel_2pore.				DR	DR PRINTS; PRO1333; 2F0REKCHANNEL.			
DR	DR InterPro; IPR001622; K+channel_pore.				DR	DR PRINTS; PRO1584; TASKCHANNEL.			
DR	DR InterPro; IPR005406; TASK1_channel.				DR	DR PRINTS; PRO1095; TASKCHANNEL.			
DR	DR InterPro; IPR003092; TASK2_channel.				KW	KW Ion transport; Ionic channel; Transmembrane; Transport.			
DR	PFam; PF00540; Ion_trans_1.				FT	FT NON_TER 1			
DR	PRINTS; PRO1333; 2F0REKCHANNEL.				FT	FT NON_TER 1			
DR	PRINTS; PRO1095; TASKCHANNEL; Transmembrane; Transport.				SQ	SEQUENCE 299 AA;	33325 MW;	CD41D8A21293904 CRC64;	
KW	Ion transport; Ionic channel; Transmembrane; Transport.				Query Match	65.3%	Score 1333;	DB 2;	Length 299;
SEQUENCE	392 AA;	43150 MW;	F5438112AAD7FB1B CRC64;		Best Local Similarity	88.9%	Pred. No. 1.6e-97;		
SEQUENCE	392 AA;	43150 MW;	F5438112AAD7FB1B CRC64;		Matches	263;	Conservative 7;	Mismatches 18;	Indels 8; Gaps 1;
Qy	1	MKRQNVRFLALIVCTFTYLVGAAFEPELITERQLRQEELARYNLSECGYE	60	Qy	4	QNRVTLALIVCTFTYLVGAAFEPELITERQLRQEELARYNLSECGYE	63		
Db	1	MKRQNVRFLALIVCTFTYLVGAAFEPELITERQLRQEELARYNLSECGYE	41	Db	2	ENVRTIALIVCTFTYLVGAAFEPELITERQLRQEELARYNLSECGYE	61		
Qy	61	ELERVLFKPHKAGVQRFAFSFYATVITLGKHAAPSNDGGKVFEMYALGIPL	120	Qy	64	RVVLRLKPHKAGVQRFAFSFYATVITLGKHAAPSNDGGKVFEMYALGIPL	123		
Db	42	ELERVLFKPHKAGVQRFAFSFYATVITLGKHAAPSNDGGKVFEMYALGIPL	101	Db	62	RVVLRLKPHKAGVQRFAFSFYATVITLGKHAAPSNDGGKVFEMYALGIPL	121		
Qy	121	TLMFQSGGERINTVRLHRAKKGMRADVSAMNVLGFPSCTSTLCIGAAAFSH	180	Qy	124	MFQSLGERINTLVRLHRAKKGMRADVSAMNVLGFPSCTSTLCIGAAAFSHYE	183		
Db	102	TLMFQSGGERINTVRLHRAKKGMRADVSAMNVLGFPSCTSTLCIGAAAFSY	161	Db	122	MFQSLGERINTFVRLHRAKKGMRADVSAMNVLGFPSCTSTLCIGAAFSY	181		
Qy	181	YEHWTFQQAYYYCPIITLTIGFEDYVALKODALQTOPQYAFSFVYILTLGTLVIGAPLN	240	Qy	184	WTFFQAYYYCPIITLTIGFEDYVALKODALQTOPQYAFSFVYILTLGTLVIGAPLN	243		
Db	182	WTFFQAYYYCPIITLTIGFEDYVALKODALQTOPQYAFSFVYILTLGTLVIGAPLN	241	Db	182	WTFFQAYYYCPIITLTIGFEDYVALKODALQTOPQYAFSFVYILTLGTLVIGAPLN	241		

Qy	244	LRFMTMNAEDEKRDAEHRAILTRNGQAAGGGG-----GSAHTTITDASSTAA 291		
Db	242	LRFMTMNAEDEKRDAEHRAILTRNGQAAGGGGCLSSGLGDGYRPRPDTCAAA 297		
RESULT 6				
Q9FSM4		PRELIMINARY;	PRT;	301 AA.
AC	Q9FSM4;			
DR	01-MAR-2001 (TREMBrel. 16, Created)			
DR	01-MAR-2001 (TREMBrel. 16, Last sequence update)			
DR	01-JUN-2003 (TREMBrel. 24, Last annotation update)			
GN	Name=KCNK3c; TWIK-related acid-sensitive K+ channel sprice variant (TASK1c).			
OS	Rattus norvegicus (Rat).			
OC	Mammalia; Metazoa; Chordata; Craniata; Euteleostomi;			
OX	Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Rattus.			
RN	[1] NCBI_TaxID=10116;			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-BOTIA;			
RA	Ohiya S., Kitakura M., Imaizumi Y.; Submitted (SPP-2000) to the EMBL/GenBank/DBJ databases.			
RL	EMBL; AB048844; BAB1671.1. -.			
DR	GO:00016021; C:intergral membrane; IEA.			
DR	GO:0005216; F:ion channel activity; IEA.			
DR	GO:0005267; F:potassium channel activity; IEA.			
DR	GO:0006813; P:potassium ion transport; IEA.			
DR	InterPro; IPR001622; K+channel_pore.			
DR	InterPro; IPR005406; TASK1_channel.			
DR	InterPro; IPR003092; TASK_Channel.			
DR	PRINTS; PRO1584; TASK1_CHANNEL.			
DR	PRINTS; PRO1095; TASKCHANNEL.			
KW	Ionic channel.			
SQ	SEQUENCE 301 AA; 32811 MW; 265DE18DFA79595B CRC64;			
Qy	Best Local Similarity 63.6%; Score 1298.5; DB 2; Length 301; Matches 256; Conservative 6; Mismatches 22; Indels 17; Gaps 2;			
Db	1 MFAALLGIPLTLMFQSGLGERINTLVYLRHAKKGMRADYSMANMVNLIGFFSCIST 170			
Qy	111 LCIGAAAFSHYENTFPQQYYCPIITLIGFDYVAQKDQLQTOQQYAFSFVYL 230			
Db	61 LCIGAAAFSHYENTFPQQYYCPIITLIGFDYVAQKDQLQTOQQYAFSFVYL 120			
Qy	231 GLTVIGAFINLVYLRFMTMNAEDKRDAEHRAILTRNGOAGGGG-----GGSATT 282			
Db	121 GLTVIGAFINLVYLRFMTMNAEDKRDAEHRAILTRNGOAGGGLSSLGIVPR 180			
Qy	283 DTASSTAA-----GGGGPRNNVYAEVLHFQSMCSCLWYKSREKLYQSYTIPMIIPRDL 333			
Db	181 DPVTCAAAGGMGVGVGSGFRNVYAEMLHFQSMCSCLWYKSREKLYQSYTIPMIIPRDL 240			
Qy	334 STSDTCVBDOSHSSPGCGGRYSDPSRRCLCSGAPRSSASSVSTGLHSIESTFGLMKRS 393			
Db	241 STSDTCVBDOSHSSPGCGGRYSDPSHPCLCSGTQRSAASSVSTGLHSIATFGLMKRS 300			
Qy	394 V 394			
Db	301 V 301			
RESULT 7				
Q63ZI0		PRELIMINARY;	PRT;	374 AA.
AC				
DR	25-OCT-2004 (TREMBrel. 28, Created)			
DR	25-OCT-2004 (TREMBrel. 28, Last sequence update)			
DR	25-OCT-2004 (TREMBrel. 28, Last annotation update)			
DE	Hypothetical protein.			

OS	Xenopus laevis (African clawed frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;			
OC	Xenopodinae; Xenopus.			
OX	NCBI_TaxID=8355;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-EYE;			
RX	PubMed=12477932; DOI=10.1073/pnas.242603899;			
RX	MEDLINE=223-1132; PubMed=12454917; DOI=10.1002/dvdy.10174;			
RA	Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.; "Genetic and genomic tools for Xenopus research: The NIH Xenopus Dev. Dyn. 225:384-391(2002).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-EYE;			
RX	PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altenschul S.P., Buetow K.H., Schaefter C.P., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scappleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheerz T.B., Brownstein M.J., Uedan O., Yoshihiko S., Carninci P., Prange C., Raha S.S., Logueblano N.A., Peters G.J., Abramson R.D., Mullahay S.J., Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Helton B., Kettenman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smilis D.E., Schnurch A., Schein J.E., Jones S.J., Marra M.A., Jones S.J., Marras M.A., DR			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Helton B., Kettenman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Jones S.J., Marra M.A., DR			
RA	Jones S.J., Marra M.A., DR			
RA	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			
RN	[13]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-EYE;			
RA	Klein S., Gerhard D.S., DR			
RA	Submitted (SBP-2000) to the EMBL/GenBank/DBJ databases.			
RL	EMBL; BC082937; AAH82937.1; -.			
DR	DR			
KW	Hypothetical protein.			
SQ	SEQUENCE 374 AA; 42718 MW; 8F37D8FF1F89F63 CRC64;			
Query Match	56.3%;	Score 1150;	DB 2;	Length 374;
Best Local Similarity	59.6%;	Pred. No. 6..6-83;		
Matches 235;	Conservative 47;	Mismatches 92;	Indels 20;	GapS 4;
RN				
RP	SEQUENCE FROM N.A.			
RC	TISSUE-EYE;			
RA	Klein S., Gerhard D.S., DR			
RA	Submitted (SBP-2000) to the EMBL/GenBank/DBJ databases.			
RL	EMBL; BC082937; AAH82937.1; -.			
KW	Hypothetical protein.			
SQ	SEQUENCE 374 AA;	42718 MW;	8F37D8FF1F89F63 CRC64;	
Query Match	56.3%;	Score 1150;	DB 2;	Length 374;
Best Local Similarity	59.6%;	Pred. No. 6..6-83;		
Matches 235;	Conservative 47;	Mismatches 92;	Indels 20;	GapS 4;
RN				
RP	SEQUENCE FROM N.A.			
RC	TISSUE-EYE;			
RA	Klein S., Gerhard D.S., DR			
RA	Submitted (SBP-2000) to the EMBL/GenBank/DBJ databases.			
RL	EMBL; BC082937; AAH82937.1; -.			
KW	Hypothetical protein.			
SQ	SEQUENCE 374 AA;	42718 MW;	8F37D8FF1F89F63 CRC64;	
Query Match	56.3%;	Score 1150;	DB 2;	Length 374;
Best Local Similarity	59.6%;	Pred. No. 6..6-83;		
Matches 235;	Conservative 47;	Mismatches 92;	Indels 20;	GapS 4;
RN				
RP	SEQUENCE FROM N.A.			
RC	TISSUE-EYE;			
RA	Klein S., Gerhard D.S., DR			
RA	Submitted (SBP-2000) to the EMBL/GenBank/DBJ databases.			
RL	EMBL; BC082937; AAH82937.1; -.			
KW	Hypothetical protein.			
SQ	SEQUENCE 374 AA;	42718 MW;	8F37D8FF1F89F63 CRC64;	
Query Match	56.3%;	Score 1150;	DB 2;	Length 374;
Best Local Similarity	59.6%;	Pred. No. 6..6-83;		
Matches 235;	Conservative 47;	Mismatches 92;	Indels 20;	GapS 4;
RN				
RP	SEQUENCE FROM N.A.			
RC	TISSUE-EYE;			
RA	Klein S., Gerhard D.S., DR			
RA	Submitted (SBP-2000) to the EMBL/GenBank/DBJ databases.			
RL	EMBL; BC082937; AAH82937.1; -.			
KW	Hypothetical protein.			
SQ	SEQUENCE 374 AA;	42718 MW;	8F37D8FF1F89F63 CRC64;	
Query Match	56.3%;	Score 1150;	DB 2;	Length 374;
Best Local Similarity	59.6%;	Pred. No. 6..6-83;		
Matches 235;	Conservative 47;	Mismatches 92;	Indels 20;	GapS 4;
RN				
RP	SEQUENCE FROM N.A.			
RC	TISSUE-EYE;			
RA	Klein S., Gerhard D.S., DR			
RA	Submitted (SBP-2000) to the EMBL/GenBank/DBJ databases.			
RL	EMBL; BC082937; AAH82937.1; -.			
KW	Hypothetical protein.			
SQ	SEQUENCE 374 AA;	42718 MW;	8F37D8FF1F89F63 CRC64;	
Query Match	56.3%;	Score 1150;	DB 2;	Length 374;
Best Local Similarity	59.6%;	Pred. No. 6..6-83;		
Matches 235;	Conservative 47;	Mismatches 92;	Indels 20;	GapS 4;
RN				
RP	SEQUENCE FROM N.A.			
RC	TISSUE-EYE;			
RA	Klein S., Gerhard D.S., DR			
RA	Submitted (SBP-2000) to the EMBL/GenBank/DBJ databases.			
RL	EMBL; BC082937; AAH82937.1; -.			
KW	Hypothetical protein.			
SQ	SEQUENCE 374 AA;	42718 MW;	8F37D8FF1F89F63 CRC64;	
Query Match	56.3%;	Score 1150;	DB 2;	Length 374;
Best Local Similarity	59.6%;	Pred. No. 6..6-83;		
Matches 235;	Conservative 47;	Mismatches 92;	Indels 20;	GapS 4;
RN				
RP	SEQUENCE FROM N.A.			
RC	TISSUE-EYE;			
RA	Klein S., Gerhard D.S., DR			
RA	Submitted (SBP-2000) to the EMBL/GenBank/DBJ databases.			
RL	EMBL; BC082937; AAH82937.1; -.			
KW	Hypothetical protein.			
SQ	SEQUENCE 374 AA;	42718 MW;	8F37D8FF1F89F63 CRC64;	
Query Match	56.3%;	Score 1150;	DB 2;	Length 374;
Best Local Similarity	59.6%;	Pred. No. 6..6-83;		
Matches 235;	Conservative 47;	Mismatches 92;	Indels 20;	GapS 4;
RN				
RP	SEQUENCE FROM N.A.			
RC	TISSUE-EYE;			
RA	Klein S., Gerhard D.S., DR			
RA	Submitted (SBP-2000) to the EMBL/GenBank/DBJ databases.			
RL	EMBL; BC082937; AAH82937.1; -.			
KW	Hypothetical protein.			
SQ	SEQUENCE 374 AA;	42718 MW;	8F37D8FF1F89F63 CRC64;	
Query Match	56.3%;	Score 1150;	DB 2;	Length 374;
Best Local Similarity	59.6%;	Pred. No. 6..6-83;		
Matches 235;	Conservative 47;	Mismatches 92;	Indels 20;	GapS 4;
RN				
RP	SEQUENCE FROM N.A.			
RC	TISSUE-EYE;			
RA	Klein S., Gerhard D.S., DR			
RA	Submitted (SBP-2000) to the EMBL/GenBank/DBJ databases.			
RL	EMBL; BC082937; AAH82937.1; -.			
KW	Hypothetical protein.			
SQ	SEQUENCE 374 AA;	42718 MW;	8F37D8FF1F89F63 CRC64;	
Query Match	56.3%;	Score 1150;	DB 2;	Length 374;
Best Local Similarity	59.6%;	Pred. No. 6..6-83;		
Matches 235;	Conservative 47;	Mismatches 92;	Indels 20;	GapS 4;
RN				
RP	SEQUENCE FROM N.A.			
RC	TISSUE-EYE;			
RA	Klein S., Gerhard D.S., DR			
RA	Submitted (SBP-2000) to the EMBL/GenBank/DBJ databases.			
RL	EMBL; BC082937; AAH82937.1; -.			
KW	Hypothetical protein.			
SQ	SEQUENCE 374 AA;	42718 MW;	8F37D8FF1F89F63 CRC64;	
Query Match	56.3%;	Score 1150;	DB 2;	Length 374;
Best Local Similarity	59.6%;	Pred. No. 6..6-83;		
Matches 235;	Conservative 47;	Mismatches 92;	Indels 20;	GapS 4;
RN				
RP	SEQUENCE FROM N.A.			
RC	TISSUE-EYE;			
RA	Klein S., Gerhard D.S., DR			
RA	Submitted (SBP-2000) to the EMBL/GenBank/DBJ databases.			
RL	EMBL; BC082937; AAH82937.1; -.			
KW	Hypothetical protein.			
SQ	SEQUENCE 374 AA;	42718 MW;	8F37D8FF1F89F63 CRC64;	
Query Match	56.3%;	Score 1150;	DB 2;	Length 374;
Best Local Similarity	59.6%;	Pred. No. 6..6-83;		
Matches 235;	Conservative 47;	Mismatches 92;	Indels 20;	GapS 4;
RN				
RP	SEQUENCE FROM N.A.			
RC	TISSUE-EYE;			
RA	Klein S., Gerhard D.S., DR			
RA	Submitted (SBP-2000) to the EMBL/GenBank/DBJ databases.			
RL	EMBL; BC082937; AAH82937.1; -.			
KW	Hypothetical protein.			
SQ	SEQUENCE 374 AA;	42718 MW;	8F37D8FF1F89F63 CRC64;	
Query Match	56.3%;	Score 1150;	DB 2;	Length 374;
Best Local Similarity	59.6%;	Pred. No. 6..6-83;		
Matches 235;	Conservative 47;	Mismatches 92;	Indels 20;	GapS 4;
RN				
RP	SEQUENCE FROM N.A.			
RC	TISSUE-EYE;			
RA	Klein S., Gerhard D.S., DR			
RA	Submitted (SBP-2000) to the EMBL/GenBank/DBJ databases.			
RL	EMBL; BC082937; AAH82937.1; -.			
KW	Hypothetical protein.			
SQ	SEQUENCE 374 AA;	42718 MW;	8F37D8FF1F89F63 CRC64;	
Query Match	56.3%;	Score 1150;	DB 2;	Length 374;
Best Local Similarity	59.6%;	Pred. No. 6..6-83;		
Matches 235;	Conservative 47;	Mismatches 92;	Indels 20;	GapS 4;
RN				
RP	SEQUENCE FROM N.A.			
RC	TISSUE-EYE;			
RA	Klein S., Gerhard D.S., DR			
RA	Submitted (SBP-2000) to the EMBL/GenBank/DBJ databases.			
RL	EMBL; BC082937; AAH82937.1; -.			
KW	Hypothetical protein.			
SQ	SEQUENCE 374 AA;	42718 MW;	8F37D8FF1F89F63 CRC64;	
Query Match	56.3%;	Score 1150;	DB 2;	Length 374;
Best Local Similarity	59.6%;	Pred. No. 6..6-83;		
Matches 235;	Conservative 47;	Mismatches 92;	Indels 20;	GapS 4;
RN				
RP	SEQUENCE FROM N.A.			
RC	TISSUE-EYE;			
RA	Klein S., Gerhard D.S., DR			
RA				

RESULT 8		HUMAN		STANDARD;		PRT;		374 AA.	
P	C	C	C	C	C	C	C	C	C
P	P	CW9 HUMAN							
P	P	Q9NC2;							
P	P	16-CTT-2001	(Rel. 40, Created)						
P	P	16-OCT-2001	(Rel. 40, Last sequence update)						
P	P	05-JUL-2004	(Rel. 44, Last annotation)						
P	P	potassium channel K member 9	(Acid-sensitive potassium channel protein TASK-3)						
P	P	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo sapiens (Human); Metazoa; Chordata; Craniata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo sapiens (Human); Synonyms=TASK3;							
P	P	NAME=KCNK9; Synonyms=TASK3;							
P	P	Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo sapiens (Human);							
P	P	"TASK-3, a novel tandem pore domain acid-sensitive K <sup>+</sup> channel. An extracellular histidine as pH sensor.";							
P	P	J. Biol. Chem. 275:16650-16657(2000).							
P	P	[1]							
P	P	SEQUENCE FROM N.A.							
P	P	TISSUE=Cerebellum;							
P	P	PubMed=10287530; DOI=10.1016/S0169-328X(00)00183-2;							
P	P	Raihan S., Wischmeyer E., Liu G.X., Preisig-Mueller R., Daut J., Karachan A., Derst C.,							
P	P	"TASK-3, a novel tandem pore domain acid-sensitive K <sup>+</sup> channel. An extracellular histidine as pH sensor.";							
P	P	J. Biol. Chem. 275:16650-16657(2000).							
P	P	[2]							
P	P	SEQUENCE FROM N.A.							
P	P	TISSUE=Cerebellum;							
P	P	PubMed=11042355; DOI=10.1016/S0169-328X(00)00183-2;							
P	P	Chamoun C.G., Meadows H.J., Godden R.J., Campbell D.A., Duckworth M., Keell R.B., Murdoch P.R., Randall A.D., Remnie G.I., Gloster I.S.;							
P	P	"Cloning, localisation and functional expression of a novel human, cerebellum specific, two pore domain potassium channel.";							
P	P	Brain Res. Mol. Brain Res. 82:74-83 (2000).							
P	P	[3]							
P	P	SEQUENCE FROM N.A.							
P	P	Girard C., Legeay F., Tinel N., Lazardinski M.,							
P	P	"Human Task-3, a novel 2p domain potassium channel related to Task.";							
P	P	Submitted (JUN-2000) to the ENMBL/GenBank/DDJB/GenBank databases.							
P	P	[4]							
P	P	SEQUENCE FROM N.A.							
P	P	Medline=21324619; PubMed=11431495;							
P	P	Vega-Saenz de Miera E., Lau D.H.P., Zhadina M., Pontney D., Coetzee W.A., Rudy B.,							
P	P	"K <sup>+</sup> T3.2 and K <sup>+</sup> T3.3, two novel human two-pore K(+) channels closely related to TASK-1";							
P	P	J. Neurophysiol. 86:130-142 (2001).							
P	P	-1- FUNCTION: pH-dependent, voltage-insensitive, background potassium channel protein.							
P	P	-1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).							
P	P	-1- TISSUE SPECIFICITY: Mainly found in the cerebellum. Also found in diencephalon, gland, kidney and lung.							
P	P	-1- MISCELLANEOUS: Inhibited by phorbol 12-myristate 13-acetate (PMA).							
P	P	-1- INSensitivity to changes in the pH range of 7-8.							
P	P	-1- SIMILARITY: Belongs to the two pore domain potassium channel (TC 1.A.1.8) family.							
R	R	C	C	C	C	C	C	C	C
R	R	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce">http://www.isb-sib.ch/announce</a> or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).							
R	R	EMBL; AF212829; AAF37081; -;							
R	R	EMBL; AF228824; AAC31730; -;							
R	R	EMBL; AF227980; AAF65982; -;							

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EMBL: AF212829; AAF63708; -;  
EMBL: AF248241; AAG31730; -;  
EMBL: AF279809; AAF85982; -;

OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Qy	299 VYAEVILHPOSMCSCLWIKSREKLQYSIPMIIPRDLSSTDTCVEOSHSSPGGGRRYSDTPS	358
OX	Mammalia; Eutheria; Rodentia; Caviidae; Cavia.	Db	292 -----DLQSVCSACVRSQP--QNFQATLAPOLHSISCRIEI-----SPS	331
RN	[1]			
RC	SEQUENCE FROM N.A.			
TISSUE=brain;				
MEDLINEID=20087530; PubMed=10747866; DOI=10.1074/jbc.M000030200;		Qy	359 RRCICSGAPRSAISVSVTGLHSLSLSTFRGLMKRESSV	394
RAJAN S., Wieschmeyer E., Liu G.X., Preisig-Muelle R., Daut J.,		Db	332 -TIKNSLFPSPISVSFOLHSFQDNHMLRKS	365
RAS	Karschin A., Derbt C.;			
RT	"TASK-3, a novel tandem pore domain acid-sensitive K+ channel. An extracellular histidine as pH sensor".			
RL	J. Biol. Chem. 275:16650-16657 (2000)			
CC	-I- FUNCTION: pH-dependent, voltage-insensitive, background potassium channel protein.			
CC	-I- SIMILARITY: Belongs to the two pore domain potassium channel (TC 1.A.1.8) family.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).			
CC	EMBL: AP212827; AACF63706.1; -			
DR	InterPro; IPR005821; Ion trans.			
DR	InterPro; IPR003280; K+channel_pore.			
DR	InterPro; IPR001622; K+channel_pore.			
DR	InterPro; IPR005407; TASK3 channel.			
DR	InterPro; IPR003092; TASK_channel.			
DR	Pfam; PF00520; Iontrans_1.			
DR	PRINTS; PRO1333; 2PORECHANEL.			
DR	PRINTS; PRO1585; TASKCHANNEL.			
DR	PRINTS; PRO1095; TASKCHANNEL.			
KW	Glycoprotein; Ion transport; Ionic channel; Potassium; Potassium channel; Transmembrane; Transport; Voltage-gated channel.			
DOMAIN	1 DOMAIN 8			
FT	TRANSMEM 9 29			
FT	TRANSMEM 78 101			
FT	TRANSMEM 108 128			
FT	TRANSMEM 129 158			
FT	TRANSMEM 159 179			
FT	TRANSMEM 184 207			
FT	TRANSMEM 219 239			
FT	TRANSMEM 240 365			
FT	CARBONYD 53 53			
SEQ	SEQUENCE 365 AA; 40769 NW; 261DC973FF53AF91 CRC64;			
Query Match	52.4% ; Score 1069.5; DB 1; Length 365;			
Best Local Similarity	57.1%; Pred. No. 1.e-76; Mismatches 43; Indels 33; Gaps 6;			
Matches	226; Conservative			
Qy	1 MKEQNVRITLAVTCTFTYLGVAFVDALESEPELIERQRQLQEELARYNLSQLGYYE 60	Qy	1 MKEQNVRITLAVTCTFTYLGVAFVDALESEPELIERQRQLQEELARYNLSQLGYYE 60	60
Db	1 MKEQNVRITLAVTCTFTYLGVAFVDALESEPELIERQRQLQEELARYNLSQLGYYE 60	Db	1 MKEQNVRITLAVTCTFTYLGVAFVDALESEPELIERQRQLQEELARYNLSQLGYYE 60	60
Qy	61 ELERVVFLPKPHKAGVWRFAGSFYFAITVITIGYGHAAAPSTDGGKVFCMFYALIGGPL 120	Qy	61 ELERVVFLPKPHKAGVWRFAGSFYFAITVITIGYGHAAAPSTDGGKVFCMFYALIGGPL 120	120
Db	61 QLELVILQSEPHRAVGQVKPAGSFYFAITVITIGYGHAAAPGTDAFGKFCMFYAVLGPL 120	Db	61 QLELVILQSEPHRAVGQVKPAGSFYFAITVITIGYGHAAAPGTDAFGKFCMFYAVLGPL 120	120
Qy	.121 TLVMFQSLGERINTLVRLLHRAKKGLGRADVSMAANVLIGFFSCSSTLCGAALFSH 180	Qy	.121 TLVWFQSLGERINTLVRLLHRAKKGLGRADVSMAANVLIGFFSCSSTLCGAALFSH 180	180
Db	.121 TLVWFQSLGERINTLVRLLHRAKKGLGRADVSMAANVLIGFFSCSSTLCGAALFSH 180	Db	.121 TLVWFQSLGERINTLVRLLHRAKKGLGRADVSMAANVLIGFFSCSSTLCGAALFSH 180	180
Qy	181 YEHWTFFQAYYYCPTLTIGFQDLYVALQKDQALQTQPOYVAASFVYLTGTLTIGAPLN 240	Qy	181 YEHWTFFQAYYYCPTLTIGFQDLYVALQKDQALQTQPOYVAASFVYLTGTLTIGAPLN 240	240
Db	181 CEWSPPFHAYYYCPTLTIGFQDLYVALQKDQALQTQPOYVAASFVYLTGTLTIGAPLN 240	Db	181 CEWSPPFHAYYYCPTLTIGFQDLYVALQKDQALQTQPOYVAASFVYLTGTLTIGAPLN 240	240
Qy	241 LYVLFREMTNAEDKRDAEHRALLTRNGAOGGGGGSSAHTDTASSTA - AGGGGFRN 298	Qy	241 LYVLFREMTNAEDKRDAEHRALLTRNGAOGGGGGSSAHTDTASSTA - AGGGGFRN 298	298
Db	241 LYVLFREMTNAEDKRDAEHRALLTRNGAOGGGGGSSAHTDTASSTA - AGGGGFRN 298	Db	241 LYVLFREMTNAEDKRDAEHRALLTRNGAOGGGGGSSAHTDTASSTA - AGGGGFRN 298	298
Qy	241 LYVLFREMTNAEDKRDAEHRALLTRNGAOGGGGGSSAHTDTASSTA - AGGGGFRN 298	Qy	241 LYVLFREMTNAEDKRDAEHRALLTRNGAOGGGGGSSAHTDTASSTA - AGGGGFRN 298	298
Db	241 LYVLFREMTNAEDKRDAEHRALLTRNGAOGGGGGSSAHTDTASSTA - AGGGGFRN 298	Db	241 LYVLFREMTNAEDKRDAEHRALLTRNGAOGGGGGSSAHTDTASSTA - AGGGGFRN 298	298
RESULT	11			
Q9JLD4				







SEQUENCE FROM N.A.  
STRAIN=Bristol N2; PubMed=9851916;  
RN WormBase Consortium;  
RG "Genome sequence of the nematode *C. elegans*: a platform for investigating biology. The *C. elegans* Sequencing Consortium.";  
RR Science 282:2012-2018 (1998).  
RN [12]  
SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RA Murray J., Wohldmann P., O'Neal D.;  
RR "The sequence of *C. elegans* cosmid P24D6.";  
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
RN [13]  
SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RA Waterson R.;  
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
RN [14]  
SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RA Wilson R.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
RN [15]  
SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RG WormBase Consortium;  
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.  
RN [6]  
SEQUENCE FROM N.A.  
RA Wang Z.-W., Salkoff L.;  
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.  
RN [7]  
SEQUENCE FROM N.A.  
RG MEDLINE=22896676; PubMed=14534247;  
RA de la Cruz I.P., Levin J.Z., Cummins C., Anderson P., Horvitz H.R.;  
RR "sup-9, sup-10, and unc-93 may encode components of a two-pore K+ channel that coordinates muscle contraction in *Caenorhabditis elegans*.";  
RL J. Neurosci. 23:9133-9145 (2003).  
RN [8]  
SEQUENCE FROM N.A.  
RA Perez de la Cruz I., Horvitz H.R.;  
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: Belongs to the two pore domain potassium channel (TC 1.A.1.8.) family.  
CC EMBL: AF025454; AAC71151.2;  
EMBL: AF083652; AAC32863.1;  
DR GO: GO:0006811; P:ion transport; IEA.  
DR InterPro: IPR005221; Ion trans.  
DR InterPro: IPR003280; K+channel\_2pore.  
DR InterPro: IPR001622; K+channel\_pore.  
DR InterPro: IPR003192; TASK\_channel.  
DR Pfam: PF00520; Ion\_trans; 1.  
DR PRINTS: PRO1333; 2PORECHANEL.  
DR PRINTS: PRO1095; TASKCHANNEL.  
KW Ion transport; Ionic channel; Transmembrane; Transport.  
SQ SEQUENCE 329 AA; 36992 MW;

Db 1 MCRQNIRTLIVCTFTYLVGAAVFDALLETEENILQRKLVQVRERKLTCKNMNADYE 60  
61 ELERVVRLIKPHAKGAVQVRFAGSFYFAITVITTYGYGHAAAPSTGGKVFCMFTALLGIP 120  
61 ILEATIVKSVPHKAGYQMKSGAFYFATVITTYGYGHISTPMTAGKVFCMLYLAGIPL 120  
121 TIWVFQSLGERINTLVRYLLHAKKGIGMRRADVSMMANVLIGFSCS1STLC1-GAAAF 178  
121 GLIMFOSIGERINTLVRYLLHAKKGIGMRRADVSMMANVLIGFSCS1STLC1-GAAAF 178  
Db 121 GLIMFOSIGERINTLVRYLLHAKKGIGMRRADVSMMANVLIGFSCS1STLC1-GAAAF 177  
QY 179 SHYEHWTPFOAYYYCPITLTCGPDYTAQDQALQTPOQYTFASPVYLTGLTIVGAF 238  
178 SSYENWTYFDAVYYCFVTLTTIGFDYVAQLRGSLSQTQPEVYFSLVFLPGTVISRA 237  
239 LNIVVLRMLTMNADEKRDAEHL---LTRNGQAAGGGGGSAAHTTDASSTAAAGG 294  
238 MNLLVRLRLLMTEDERDEQEALIAAGLVRGDPTADDDFRLPLSDNVSLAS---- 292  
295 GFRNYYAEVLHFQSMCSCLYWSREKLOYSIPMI1PDLSTSPTCVEQSHSSPGGG 350  
Db 293 -----CSC-YQLPDEKLHR-----HRKHTEPHGG 316

Search completed: July 13, 2005, 08:44:33  
Job time : 92.0757 secs

Query Match 40.2%; Score 820; DB 2; Length 329;  
Best Local Similarity 48.3%; Pred. No. 8.8e-57;  
Matches 172; Conservative 54; Mismatches 84; Indels 46; Gap 7;  
SQ 1 MCRQNIRTLIVCTFTYLVGAAVFDALLETEENILQRKLVQVRERKLTCKNMNADYE 60

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Copyright (c) 1993 - 2005 Compugen Ltd.	GenCore version 5.1.6	Abg29273 Novel hum Abb64375 Drosophila Aam14676 Peptide #
OM protein - protein search, using bw model		Abb33636 Peptide #
Run on:	July 13, 2005, 07:58:54 ; Search time 97 2039 Seconds (without alignment)	Am27095 Peptide # Abb28454 Peptide # Abb19091 Protein #
Title:	US-09-503-089A-5	Aam66810 Human bon Aam54409 Human bra
Perfect score:	2042	Abg48478 Human liv Aam02399 Peptide #
Sequence:	1 MKRQNRVRLALIVCTFTYLL.....STGHSLSTFRGLMKRRSSV 394	Abg36465 Human pep Aab31804 Amino aci Abb71787 Drosophil Abo14995 Human NOV
Scoring table:	BLOSUM62	Aab31805 Amino aci Abo84626 Mouse can Aae10342 Murine TR Aay30648 A mechani Aay28497 Mouse h-T
Gapopen:	10.0 , Gapext 0.5	
Searched:	2105632 seqs, 386760381 residues	
Total number of hits satisfying chosen parameters:	2105692	
Minimum DB seq length:	0	
Maximum DB seq length:	2000000000	
Post-processing:	Minimum Match 0% Maximum Match 100%	
	Listing first 45 summaries	
Database :	A_Geneseq_16Dec04:*	RESULT 1 ID AAE10343 standard; protein; 394 AA.
	1: GeneseqP19808:*	XX
	2: GeneseqP19908:*	AC
	3: GeneseqP20008:*	XX
	4: GeneseqP20018:*	DT
	5: GeneseqP20028:*	10-DEC-2001 (first entry)
	6: GeneseqP20038:*	XX
	7: GeneseqP20048:*	DE
	8: GeneseqP20048:*	Murine TASK potassium channel protein.
Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	KW Murine; potassium channel protein; TREK-1; TASK; anaesthetic; analgesia; amnesia.
		XX
		OS Mus sp.
		XX
		PN WO200047738-A2.
		XX
		PD 17-AUG-2000.
		XX
		PF 11-FEB-2000; 2000WO-1B0003226.
		XX
		PR 12-FEB-1999; 99US-0119727P.
		PR 11-FEB-2000; 2000US-00503089.
		XX
		(CNRS ) CNRS CENT NAT RECH SCI.
		XX
		Lazdunski M, Honore E, Lescage F, Romey G, Patel AJ,
		PI XX
		DR 2000-549146/50.
		XX
		PT Novel nucleic acid encoding a TREK-1 potassium channel protein for PT transfecting cells to be used to identify compounds with anesthetic properties.
		PT XX
		PT Claim 23; Page 34-35; 39pp; English.
		PS
		CC The invention relates to human and mouse TREK-1 potassium channel proteins and their corresponding DNA molecules. TREK-1 nucleic acid is useful for transfecting cells to induce expression of the TREK-1 CC proteins and their corresponding DNA molecules. These cells are then used in assays to CC potassium channel protein. These cells are then used in assays to CC identify compounds which have anaesthetic properties, producing a safe, CC reversible state of unconsciousness with concurrent amnesia and analgesia, CC in a mammal upon inhalation. The present sequence is murine TASK CC potassium channel protein related to the invention
		XX
		SQ Sequence 394 AA;
		Query Match 100.0%; Score 2042; DB 3; Length 394;

XX	WPI; 2000-376187/32.
DR	N-PDB; AAA27746.
XX	New nucleic acid encoding a non-inactivating outwardly rectifying potassium transport channel, designated TASK2, useful in the treatment of hypertension or dysfunctions of the kidney, liver or pancreas.
PT	PT
PT	PT
PT	PT
XX	Disclosure; Fig 8; 91pp; English.
PS	
XX	The present sequence is that of human TASK1 (TWIK-related acid-sensitive K+ channel), a member of a new family of 2P domain potassium channels, also including TWIK-1 (see AAY79673) and novel TASK2 (see AAY79675). TASK1 is expressed in many different tissues, and at particularly high levels in pancreas and placenta. Host cells expressing TWIK1 family members can be used to screen for substances that modulate the activity of members of the TWIK-1 family of potassium channels. The drugs identified may be useful in the treatment of diseases of the heart or of the nervous system, such as epilepsy, arrhythmia, vascular diseases, neurodegenerative diseases, kidney, liver or pancreas diseases, hypertension, diseases associated with ischaemia or anaemia, endocrine diseases associated with anomalies of hormone secretion, and muscle diseases
CC	CC
XX	Sequence 394 AA;
SQ	Query Match 100.0%; Score 2042; DB 3; Length 394; Best Local Similarity 100.0%; Pred. No. 5.3e-213; Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Db	1 MKRQVTRLALIVCFPTTYLRAKGLGRADYSMANNVLIGFSC1STLIGAAAFSH 60 1 MKRQVTRLALIVCFPTTYLRAKGLGRADYSMANNVLIGFSC1STLIGAAAFSH 180
Qy	1 YEHWTFFQAYYYCFTLTTGFDGYVALQDQALOTPOXVAFSFYVITLGLTVGAFIN 240 1 YEHWTFFQAYYYCFTLTTGFDGYVALQDQALOTPOXVAFSFYVITLGLTVGAFIN 240
Db	241 LVVLERFMTRNNAEDEKRDAEHRALILTRNGQAGGGGGSAAHTTDASSTAAGGGGERNVTY 300 241 LVVLERFMTRNNAEDEKRDAEHRALILTRNGQAGGGGGSAAHTTDASSTAAGGGGERNVTY 300
Qy	301 AEVLHFQSNCSCLNKVSREKLQYSPLMI1PRDLSTSDFTEQSHSSPGGGRYSDTPSRR 360 301 AEVLHFQSNCSCLNKVSREKLQYSPLMI1PRDLSTSDFTEQSHSSPGGGRYSDTPSRR 360
Db	361 CLCGSAPRAISSVSTGLHSLSFRGLMKRSSLV 394 361 CLCGSAPRAISSVSTGLHSLSFRGLMKRSSLV 394
XX	RESULT 2 AAY79674 Standard: protein; 394 AA.
Db	AAY79674 Human potassium channel TASK1.
XX	TASK1; TWIK-related acid-sensitive K+ channel 1; human; potassium channel; drug screening; hypertension; hypotensive; epilepsy; arrhythmia; vascular disease; neurodegenerative disease; ischaemia; anaemia; endocrine disease; muscle disease; therapy.
XX	Homo Sapiens.
Key	Location/Qualifiers
Modified-site	53 /note= "N-glycosylated"
Modified-site	323 /note= "O-phosphorylated"
Modified-site	383 /note= "O-phosphorylated"
Modified-site	392 /note= "O-phosphorylated"
Modified-site	393 /note= "O-phosphorylated"
FT	RESULT 3 AAY7291 ID AAY7291 standard; protein; 394 AA.
FT	XX
FT	AC AAY7291;
FT	XX
FT	XX
FT	DT 11-MAY-2000 (first entry)
FT	DE Human signal peptide containing protein HSPP-68 SEQ ID NO:68.
FT	KW signal peptide-containing protein; HSPP; diagnosis; cancer;
FT	KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;
FT	KW antimicrobial; nootropic; neuroprotective; cardio-protective; hepatotropic;
FT	KW antiallergic; antidiabetic; antihistaminic; analgesic; antipyretic;
FT	(CNRS ) CNRS CENT NAT RECH SCI.
FT	Duprat, F., Lescage, E., Lazdunski, M.
FT	WO-00027871-A2.
FT	18-MAY-2000.
FT	09-NOV-1999; 99WO-IB001886.
FT	08-NOV-1999; 99US-00436265.



PT preventing, diagnosing and treating e.g. cancers, Alzheimer's disease and cardiovascular disorders.

PT Disclosure; SEQ ID NO 17; 638pp; English.

XX

The invention relates to TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611, IC47615, HNMDA-1, TWIK-9, alpha-2delta-4, 54414 and 53763 ion channel (ICP) nucleic acids and proteins. The TWIK-6, TWIK-7, IC47611, IC47615, HNMDA-1, TWIK-9, alpha-2delta-4, 54414 and 53763 ICP nucleic acids and proteins may be used for preventing, diagnosing and treating ICP-related diseases. The sequences may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of ICP proteins by expressing inactive proteins or to supplement the patients own production of ICP proteins. The proteins may also be used as antigens in the production of antibodies against ICP proteins and in assays to identify modulators of ICP protein expression and activity. The anti-ICP protein antibodies, agonists and antagonists may be used to regulate ICP protein expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of ICP proteins in samples (e.g. by immunoassay). The nucleic acids and proteins may be used to prevent, diagnose and treat a wide variety of disorders e.g. cancers and Leukaemia, Alzheimer's disease, Parkinson's disease, multiple sclerosis, epilepsy, hepatic disorders and cardiovascular disorders. This sequence represents a human protein used in the scope of the invention.

Note: The sequence data for this patent is also available in electronic format from USPTO at seqdata.uspto.gov/sequence.html.

XX

SQ Sequence 394 AA;

Query Match Score 2042; DB 8; Length 394;  
Best Local Similarity 100.0%; Pred. No. 5.3e-213;  
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MRQNVTLLAVCTFTYLLGAAVFALESPELLERQRLELROELRPELARYNLNSGGYE 60

Db 1 MRQNVTLLAVCTFTYLLGAAVFALESPELLERQRLELRRQQLRARYNLNSGGYE 60

Qy 61 ELEVVVRLKPKAGYQWYRQAFASGSFYFAITVTTIGYCHAAPSTDGKVFCMFYALIGIPL 120

Db 61 ELEVVVRLKPKAGYQWYRQAFASGSFYFAITVTTIGYCHAAPSTDGKVFCMFYALIGIPL 120

Qy 121 TLVMFQSGGERINTLVYLLHAKKGIGMRRADVSAMNVLIQFFCSITLCTIGAAAFSH 180

Db 121 TLVMFQSGGERINTLVYLLHAKKGIGMRRADVSAMNVLIQFFCSITLCTIGAAAFSH 180

Qy 181 YEHWTFFPQAYYCPILTITIGEDYVALLQDQLQLOTOPOQYTAFSFVYLTLTIVCAFLN 240

Db 181 YEHWTFFPQAYYCPILTITIGEDYVALLQDQLQLOTOPOQYTAFSFVYLTLTIVCAFLN 240

Qy 241 LVVLRFMTMNAEDEKDRAEHLRAILTRNGQAGGGGGSAHTTDASSTAAGGGFRNVY 300

Db 241 LVVLRFMTMNAEDEKDRAEHLRAILTRNGQAGGGGGSAHTTDASSTAAGGGFRNVY 300

Qy 301 AEYLHFQSMCSCLYWIKSREKLQYSIPIMTIPDLSTSPTCYBOSHSPGGGRYSDTPSRR 360

Db 301 AEYLHFQSMCSCLYWIKSREKLQYSIPIMTIPDLSTSPTCYBOSHSPGGGRYSDTPSRR 360

Qy 361 CLCGAPRSAISSVSTGHSLSLTFRGJMKRSSV 394

Db 361 CLCGAPRSAISSVSTGHSLSLTFRGJMKRSSV 394

RESULT 5  
AD127925 standard; protein; 394 AA.

XX AD127925;

AC 06-MAY-2004 (First entry)

XX Human protein #3.

DT XX

DE Human protein #3.

XX

KW Human; ion channel family; ICP; cancer; leukaemia; Alzheimer's disease; Parkinson's disease; multiple sclerosis; epilepsy; hepatic disorder; cardiovascular; antiparkinsonian; hepatotropic; nootropic; nootropic; cardiovascular.

XX Homo sapiens.

OS US2003165891-A1.

XX PD 04-SEP-2003.

XX PR 15-MAY-2002; 2002US-00146733.

XX PR 15-MAY-2002; 2002US-00146733.

XX PR 29-FEB-2000; 2000US-00515520.

XX PR 29-FEB-2000; 2000US-00515520.

XX PR 03-MAR-2000; 2000US-0185938P.

XX PR 07-APR-2000; 2000US-0195134P.

XX PR 11-APR-2000; 2000US-0195993P.

XX PR 26-APR-2000; 2000US-0195999P.

XX PR 19-SEP-2000; 2000US-0235137P.

XX PR 25-SEP-2000; 2000US-023518P.

XX PR 25-SEP-2000; 2000US-0235059P.

XX PR 15-DEC-2000; 2000US-0255240P.

XX PR 18-DEC-2000; 2000US-025588P.

XX PR 21-DEC-2000; 2000US-0255028P.

XX PR 28-FEB-2001; 2001US-00736720.

XX PR 06-APR-2001; 2001US-00838035.

XX PR 11-APR-2001; 2001US-00833081.

XX PR 25-APR-2001; 2001US-0083128.

XX PR 19-SEP-2001; 2001US-0097683.

XX PR 25-SEP-2001; 2001US-0094252.

XX PR 25-SEP-2001; 2001US-0094256.

XX PR 17-DEC-2001; 2001US-0004623.

DR WPI 2004-069000/07.

XX PA (MILL- ) MILLENIUM PHARM INC.

XX PI Curtis RAJ, Glucksmann MA, Silos-Santiago I;

XX PR 2004-069000/07.

XX PT TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611, IC47615, HNMDA-1, TWIK-9, alpha-2delta-4, 54414 and 53763 nucleic acids and proteins, useful for preventing, diagnosing and treating ICP-related diseases. The sequences may be used for preventing, diagnosing and treating e.g. cancers, Alzheimer's disease and cardiovascular disorders.

XX DR Disclosure; SEQ ID NO 18; 638PP; English.

XX The invention relates to TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611, IC47615, HNMDA-1, TWIK-9, alpha-2delta-4, 54414 and 53763 ion channel family (ICP) nucleic acids and proteins. The TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611, IC47615, HNMDA-1, TWIK-9, alpha-2delta-4, 54414 and 53763 ICP nucleic acids and proteins may be used for preventing, diagnosing and treating ICP-related diseases. The sequences may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of ICP proteins by expressing inactive proteins or to supplement the patients own production of ICP proteins. The proteins may also be used as antigens in the production of antibodies against ICP proteins and in assays to identify modulators of ICP protein expression and activity. The anti-ICP protein antibodies, agonists and antagonists may be used to regulate ICP protein expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of ICP proteins in samples (e.g. by immunoassay). The nucleic acids and proteins may be used to prevent, diagnose and treat a wide variety of disorders e.g. cancers and Leukaemia, Alzheimer's disease, multiple sclerosis, epilepsy, hepatic disorders and cardiovascular disorders. This sequence represents a human protein used in the scope of the invention.

CC CC

Best Local Similarity 100.0%; Pred. No. 5.3e-213; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKRNRVTLALIVCTFTYLVGAAVFDALESEPLIERORLERQQRERARYNLSQGYE 60  
 Db 1 MKRNRVTLALIVCTFTYLVGAAVFDALESEPLIERORLERQQRERARYNLSQGYE 60  
 QY 61 ELERVVLRLKPKHAKGVQMRFAGSFYFAITVITIGYHRAAPSTDGKVFCMFYALIGIPL 120  
 Db 61 ELERVVLRLKPKHAKGVQMRFAGSFYFAITVITIGYHRAAPSTDGKVFCMFYALIGIPL 120  
 QY 121 TLWFOQLGERINTLVRLHRAKKGMRADVISMANVNLIGFSCISTICIGAAASH 180  
 Db 121 TLWFOQLGERINTLVRLHRAKKGMRADVISMANVNLIGFSCISTICIGAAASH 180  
 QY 181 YEHTFFQAYYYCPTTLLTIGFDGYVALQDQALQTOPQYVAFSFVYLGLTVIGALN 240  
 Db 181 YEHTFFQAYYYCPTTLLTIGFDGYVALQDQALQTOPQYVAFSFVYLGLTVIGALN 240  
 QY 241 LYVLFRTMNAEDERKDAFHRLALLTRNGQAGGGGGSAHTTDATASSTAAGGGGFRNVY 300  
 Db 241 LYVLFRTMNAEDERKDAFHRLALLTRNGQAGGGGGSAHTTDATASSTAAGGGGFRNVY 300  
 QY 301 AEVLHFQSMCSCLWYKSREKLQYSIPMIPRDLSSTDTCVEQSHSSPQGGGRYSDTPERR 360  
 Db 301 AEVLHFQSMCSCLWYKSREKLQYSIPMIPRDLSSTDTCVEQSHSSPQGGGRYSDTPERR 360  
 QY 361 CLCGGAPRSAISSVSTGHLSLSTRGLMKRSSLV 394  
 Db 361 CLCGGAPRSAISSVSTGHLSLSTRGLMKRSSLV 394

**RESULT 6**

ID ADI27915 standard; protein; 395 AA.  
 XX ADI27915;  
 AC ADI27915;  
 DT 06-MAY-2004 (first entry)  
 XX Human protein #1.

XX Human; ion channel family; ICF; cancer; leukaemia; Alzheimer's disease;  
 KW Parkinson's disease; multiple sclerosis; epilepsy; hepatic disorder;  
 KW cardiovascular disorder; cytostatic; neuroprotective; nocropic;  
 KW antiparkinsonian; hepatotrophic; cardiovascular.

XX Homo sapiens.  
 PN US2003165891-A1.  
 XX 04-SEP-2003.

XX 15-MAY-2002; 2002US-00146733.

PR 29-FEB-2000; 2000US-00515520.  
 PR 29-FEB-2000; 2000US-0185938P.  
 PR 03-MAR-2000; 2000US-00518866.  
 PR 07-APR-2000; 2000US-0195734P.  
 PR 11-APR-2000; 2000US-0195939P.  
 PR 26-APR-2000; 2000US-0199799P.  
 PR 19-SEP-2000; 2000US-0233537P.  
 PR 25-SEP-2000; 2000US-0235018P.  
 PR 21-SEP-2000; 2000US-0235059P.  
 PR 15-DEC-2000; 2000US-0256240P.  
 PR 18-DEC-2000; 2000US-0256588P.  
 PR 21-DEC-2000; 2000US-028028P.  
 PR 28-FEB-2001; 2000US-008796720.  
 PR 06-APR-2001; 2001US-00828035.  
 PR 11-APR-2001; 2001US-00833081.  
 PR 25-APR-2001; 2001US-00843128.  
 PR 19-SEP-2001; 2001US-00957663.  
 PR 25-SEP-2001; 2001US-00964232.

PR 25-SEP-2001; 2001US-00964256.  
 PR 17-DEC-2001; 2001US-00024623.  
 XX (MILL-) MILLENNIUM PHARM INC.  
 XX Curtis RAJ, Glucksmann MA, Silos-Santiago I;  
 XX DR WP; 2004-069000/07.

XX TWIK-6, TWIK-7, TWIK-8, IC47611, IC47615, HNMDA-1, TWIK-9,  
 PT alpha2delta-4, 54414, or 53763 nucleic acids and proteins, useful for  
 PT preventing, diagnosing and treating e.g. cancers, Alzheimer's disease and  
 PT cardiovascular disorders.

XX Disclosure; SEQ ID NO 8; 638pp; English.

XX The invention relates to TWIK-6, TWIK-7, IC47611, IC47615, HNMDA-1, TWIK-9, alpha-2delta-4, 54414 and 53763 ion channel family (ICP) nucleic acids and proteins. The TWIK-6, TWIK-7, IC47611, IC47615, HNMDA-1, TWIK-9, alpha-2delta-4, 54414 and 53763 ICP nucleic acids and proteins may be used for preventing, diagnosing and treating ICP-related diseases. The sequences may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of ICP proteins by expressing inactive proteins or to supplement the patients own production of ICP proteins. The proteins may also be used as antigens in the production of antibodies against ICP proteins and in assays to identify modulators of ICP protein expression and activity. The anti-ICP protein antibodies, agonists and antagonists may be used to regulate ICP protein expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of ICP proteins in samples (e.g. by immunoassay). The nucleic acids and proteins may be used to prevent, diagnose and treat a wide variety of disorders, e.g. cancers and leukaemia, Alzheimer's disease, Parkinson's disease, multiple sclerosis, epilepsy, hepatic disorders and cardiovascular disorders. This sequence represents a human protein used in the scope of the invention. Note: The sequence data for this patent is also available in electronic format from USPTO at seqdata.uspto.gov/sequence.html.

SQ Sequence 395 AA;

Query Match Score 100.0%; Length 395;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-213;  
 Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRQNRVTLALIVCTFTYLVGAAVFDALESEPLIERORLERQQRERARYNLSQGYE 60  
 Db 2 MGRQNRVTLALIVCTFTYLVGAAVFDALESEPLIERORLERQQRERARYNLSQGYE 61  
 QY 61 ELERVVLRLKPKHAKGVQMRFAGSFYFAITVITIGYHRAAPSTDGKVFMCFYALIGIPL 120  
 Db 62 ELERVVLRLKPKHAKGVQMRFAGSFYFAITVITIGYHRAAPSTDGKVFMCFYALIGIPL 121  
 QY 61 TLWFOQLGERINTLVRLHRAKKGMRADVISMANVNLIGFSCISTICIGAAASH 180  
 Db 121 TLWFOQLGERINTLVRLHRAKKGMRADVISMANVNLIGFSCISTICIGAAASH 181  
 QY 181 YEWTFQQAYYCPTTLLTIGFDGYVALQDQALQTOPQYVAFSFVYLGLTVIGAFIN 240  
 Db 182 YEWTFQQAYYCPTTLLTIGFDGYVALQDQALQTOPQYVAFSFVYLGLTVIGAFIN 241  
 QY 241 LVVLFREMTMNAEDEKRDAFHRLALLTRNGQAGGGGGSAHTTDASSTAAGGGFPRNVY 300  
 Db 242 LVVLFREMTMNAEDEKRDAFHRLALLTRNGQAGGGGGSAHTTDASSTAAGGGFPRNVY 301  
 QY 301 AEWLFQSMCSCLWYKSREKLQYSIPMIPRDLSSTDTCVEQSHSSPGGGGRYSDTPSRR 360  
 Db 302 AEWLFQSMCSCLWYKSREKLQYSIPMIPRDLSSTDTCVEQSHSSPGGGGRYSDTPSRR 361  
 QY 361 CLCGGAPRSAISSVSTGHLSLSTRGLMKRSSLV 394  
 Db 362 CLCGGAPRSAISSVSTGHLSLSTRGLMKRSSLV 395

**RESULT 7**  
**ID ADI27916 standard; protein; 412 AA.**

**XX ID ADI27916;**  
**XX AC ADI27916;**  
**XX DT 06-MAY-2004 (First entry)**  
**XX DB Rat protein #1.**  
**XX KW Rat; ion channel family; ICF; cancer; leukaemia; Alzheimer's disease; Parkinson's disease; multiple sclerosis; epilepsy; hepatic disorder; cardiovascular disorder; cytosatic; neuroprotective; nootropic; antiParkinsonian; hepatotrophic; cardiovascular.**  
**XX OS Rattus norvegicus.**  
**XX PN US2003165891-A1.**  
**XX PD 04-SEP-2003.**  
**XX PR 15-MAY-2002; 2002US-00146733.**  
**XX PR 29-FEB-2000; 2000US-00515520.**  
**PR 03-MAR-2000; 2000US-0185938P.**  
**PR 07-APR-2000; 2000US-0157734P.**  
**PR 26-APR-2000; 2000US-0199799P.**  
**PR 19-SEP-2000; 2000US-021537P.**  
**PR 25-SEP-2000; 2000US-0235018P.**  
**PR 15-DEC-2000; 2000US-0256240P.**  
**PR 18-DEC-2000; 2000US-0256588P.**  
**PR 21-DEC-2000; 2000US-02558028P.**  
**PR 28-FEB-2001; 2001US-00796720.**  
**PR 11-APR-2001; 2001US-00828035.**  
**PR 25-APR-2001; 2001US-00843128.**  
**PR 25-SEP-2001; 2001US-00964252.**  
**PR 25-SEP-2001; 2001US-00964256.**  
**PR 17-DEC-2001; 2001US-00024623.**  
**XX PA (MILL-) MILLENNIUM PHARM INC.**  
**XX PI Curtiss RAJ, Glucksmann MA, Silos-Santiago I;**  
**XX DR WPI: 2004-069000/07.**  
**XX PT TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611, IC47615, HNMDA-1, TWIK-9, alpha2Delta-4, 54414, or 53763 nucleic acids and proteins, useful for preventing, diagnosing and treating e.g. cancers, Alzheimer's disease and cardiovascular disorders.**  
**XX Disclosure: SEQ ID NO 9; 638pp; English.**  
**CC The invention relates to TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611, IC47615, HNMDA-1, TWIK-9, alpha2Delta-4, 54414, or 53763 nucleic acids and proteins. The TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611, IC47615, HNMDA-1, TWIK-9, alpha2Delta-4, 54414 and S3763 ICF nucleic acids and proteins may be used for preventing, diagnosing and treating ICF-related diseases. The sequences may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of ICF proteins by expressing inactive proteins or to supplement the patients own production of ICF proteins. The proteins may also be used as antigens in the production of antibodies against ICF proteins and in assays to identify modulators of ICF protein expression and activity. The anti-ICF protein antibodies, agonists and antagonists may be used to regulate ICF protein expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of ICF proteins in**  
**samples (e.g. by immunoassay). The nucleic acids and proteins may be used to prevent, diagnose and treat a wide variety of disorders, e.g. cancers and leukemia, Alzheimer's disease, Parkinson's disease, multiple sclerosis, epilepsy, hepatic disorders and cardiovascular disorders. This sequence represents a rat protein used in the scope of the invention.**  
**Note: The sequence data for this patent is also available in electronic format from USPTO at seqdata.uspto.gov/sequence.html.**

**SQ Sequence 412 AA:**

Query	Match	Score	Length
1	MKRQVNRVTLALIVCFTTYLLVGAAYFDALSEPELIERQRLERLQQLRARNLSCGGYE	90 - 6%	412;
2	MKRQVNRVTLALIVCFTTYLLVGAAYFDALSEPELIERQRLERLQQLRARNLSCGGYE	88 - 3%	412 - 192;
Qy	ELERVYVLRLEPHKAGQWRFAGSFYFAITVTTTCGYHAAPSTDGSKVFCMFYALLGIP	Best Local Similarity	Pred. No. 4.1e-192;
Db	ELERVYVLRLEPHKAGQWRFAGSFYFAITVTTTCGYHAAPSTDGSKVFCMFYALLGIP	Matches	Mismatches
Qy	ELERVYVLRLEPHKAGQWRFAGSFYFAITVTTTCGYHAAPSTDGSKVFCMFYALLGIP	61	23;
Db	ELERVYVLRLEPHKAGQWRFAGSFYFAITVTTTCGYHAAPSTDGSKVFCMFYALLGIP	62	17;
Qy	TLVMPFSLGERINTLVYLHRAKEGLGMGRADYSMANMVNLIGFSCLISTLCIGAAFSH	Score	Gaps
Db	TLVMPFSLGERINTLVYLHRAKEGLGMGRADYSMANMVNLIGFSCLISTLCIGAAFSH	90 - 3%	2;
Qy	YEHWTFFQAYYYCFITLTGFDVQLDQALQTQVTAFAFSVYVILTGLTVGAFLN	Score	Indels
Db	YERWTFQAYYYCFITLTGFDVQLDQALQTQVTAFAFSVYVILTGLTVGAFLN	181	240;
Qy	IUVLIREPMTNNAEDEKDAEHRLATTRNGQAGGGCG-----GCSAHTTDTASSTAAA-	Score	;
Db	IUVLIREPMTNNAEDEKDAEHRLATTRNGQAGGGCG-----GCSAHTTDTASSTAAA-	241	291;
Qy	GGGCPGGGRYSDTPSRRCLGAPSRAISSVSTGHSLSTERGIMKRRSSV	Score	;
Db	GGGCPGGGRYSDTPSRRCLGAPSRAISSVSTGHSLSTERGIMKRRSSV	344	394;
Qy	AAY95230 standard; protein; 405 AA.	Score	;
Db	AAY95230 standard; protein; 405 AA.	362	412.

**RESULT 8**  
**ID AAY95230**  
**XX AC AAY95230;**  
**XX DR 29-AUG-2000 (First entry)**  
**XX DE Mouse potassium channel TASK.**  
**XX KW TASK; TWIK-related acid-sensitive K<sup>+</sup> channel; mouse; potassium channel; drug screening; hypertension; hypotensive; epilepsy; arrhythmia; vascular diseases; neurodegenerative disease; ischaemia; anoxia; endocrine disease; muscle disease; therapy.**  
**XX OS Mus musculus.**  
**XX Key Location/Qualifiers**  
**Key Modified-site**  
**FT FT /note= "N-glycosylated"**  
**FT FT /note= "O-phosphorylated"**  
**FT FT /note= "O-phosphorylated"**  
**FT FT /note= "O-phosphorylated"**  
**FT FT /note= "O-phosphorylated"**  
**XX PD WO2000027871-A2.**  
**XX PN**

XX 09-NOV-1999; 99WO-IB001886.  
 XX PR 09-NOV-1998; 98US-0107692P.  
 PR 08-NOV-1999; 99US-00436255.  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 XX Duprat F, Lebagne F, Lazardinski M;  
 XX DR; 2000-376487/32.  
 XX PR potassium acid encoding a non-inactivating outwardly rectifying potassium transport channel, designated TASK2, useful in the treatment of hypertension or dysfunctions of the kidney, liver or pancreas.  
 XX Disclosure; Fig 8; 91pp; English.  
 XX The present sequence is that of murine TASK (TWIK-related acid-sensitive K<sup>+</sup> channel), a member of a new family of 2P domain potassium channels also including human TWIK-1 (see AAY79673), human TASK1 (see AAY79674) and novel human TASK2 (see AAY79675). Human and mouse TASK proteins share 85% identity, indicating that they are products of orthologue genes. Host cells expressing TWIK-1 family members can be used to screen for substances that modulate the activity of members of the TWIK-1 family of potassium channels. The drugs identified may be useful in the treatment of diseases of the heart or of the nervous system, such as epilepsy, arrhythmias, vascular diseases, neurodegenerative diseases, kidney, liver or pancreas diseases, hypertension, diseases associated with ischaemia or anoxia, endocrine diseases associated with anomalies of hormone secretion, and muscle diseases  
 XX Sequence 405 AA;  
 SQ Query Match 89.1%; Score 1819; DB 3; Length 405;  
 Best Local Similarity 88.1%; Pred. No. 1..1e-180;  
 Matches 357; Conservative 9; Mismatches 25; Indels 14; Gaps 2;  
 Db 4 QNVRTLAIIVCTPYLLGAAYDALESEPELTERQNLRLQELRARNYLQGGYEELE 63  
 1 ENVTRLAIIVCTPYLLGAAYDALESEPELTERQNLRLQELRARNYLSEGYYEELE 60  
 Qy 64 RIVVRLKPHKAGYQWRFAGSFYFAITVTTIGYHAAPSTDGKVFCYALGIPILV 123  
 Db 61 RIVVRLKPHKAGYQWRFAGSFYFAITVTTIGYHAAPSTDGKVFCYALGIPILV 120  
 Qy 124 MFQSLGERINTLYRLHRAKGSLGMRAVDVSMANMYLIGFFSCISTICGAAAFSHYEH 183  
 Db 121 MFQSLGERINTLYRLHRAKGSLGMRAEVSMANMYLIGFFSCISTICGAAAFSYER 180  
 Qy 164 WTPFOAQTYCFCINLTIGFDTYALQKQALQTQPOVYAFSTFYVYLQGLTIGAFLNLYV 243  
 Db 181 WTPFOAQTYCFCITLTIGFDTYALQKQALQTQPOVYAFSTFYVYLQGLTIGAFLNLYV 240  
 Qy 244 LRFMTMNEDEKDAEHLALLTNGQACGGG-----GGSAHTTDASSTAA----- 291  
 Db 241 LRFMTMNEDEKDAEHLALLTNGQACGGG-----GGSAHTTDASSTAA----- 290  
 Qy 292 --GGGGFPRNNVAEVLHFSQMSMCISLWYKSRKLCYQSTIMIIIPRLSTSPTCVBOSHSSPGG 349  
 Db 301 GVGSGSPNNVAEVLHFSQMSMCISLWYKSRKLCYQSTIMIIIPRLSTSPTCVBOSHSSPGG 360  
 Qy 350 GFRYSQDTPSRRCLCSCGARSAAISSVSTLHSLSLSPRGMLKRSSV 394  
 Db 361 GGRYSQDTPSRRCLCSCGARSAAISSVSTLHSLSLAFRGMLKRSSV 405  
 Qy -  
 Db -  
 DT 21-NOV-2001 (first entry)  
 XX Mouse 2P channel protein #1.  
 DE KW Transmembrane potassium ion channel protein; inward potassium flux; pest control; membrane potential; pesticide; antihermaphrodite; nematode; insect; 2P channel; mouse.  
 XX OS Mus musculus.  
 XX PN WO200161006-A2.  
 XX PD 23-AUG-2001.  
 XX PP 14-FEB-2001; 2001WO-US004680.  
 PS PR 15-FEB-2000; 2000US-00503849.  
 XX PA (BADI ) BASF CORP.  
 PA Pausch MH;  
 XX DR WPI: 2001-5316570/59.  
 DR N-PSDB; AAS12179.  
 XX PT New polypeptide, a mutant potassium ion channel protein for improving inward potassium flux under acidic conditions.  
 CC PT Example 18; Page 53; 131pp; English.  
 CC PS Example 18; Page 53; 131pp; English.  
 CC XX The invention relates to a mutant potassium ion channel protein, having a four membrane spanning domains and two pore forming domains, comprising a mutation at the second pore forming domain. The expression of the mutant protein in a cell confers improved inward potassium flux and the ability to grow in the presence of potassium. Mutant proteins and their corresponding polynucleotide sequences can therefore be used to improve inward potassium flux into cells under acidic conditions by modulating the membrane potential using therapeutic agents. The sequences may be used to develop agonists and antagonists of potassium channel proteins in order to control pests such as nematodes and insects. This sequence represents a mouse 2P channel protein  
 SQ Sequence 309 AA;  
 Query Match 60.5%; Score 1235.5; DB 4; Length 309;  
 Best Local Similarity 83.9%; Pred. No. 2..6e-125;  
 Matches 250; Conservative 8; Mismatches 27; Indels 13; Gaps 3;  
 Qy 4 QNVRTLAIIVCTPYLLGAAYDALESEPELTERQNLRLQELRARNYLQGGYEELE 63  
 Db 13 ENVTRLAIIVCTPYLLGAAYDALESEPELTERQNLRLQELRARNYLSEGYYEELE 72  
 Qy 64 RIVVRLKPHKAGYQWRFAGSFYFAITVTTIGYHAAPSTDGKVFCYALGIPILV 123  
 Db 61 RIVVRLKPHKAGYQWRFAGSFYFAITVTTIGYHAAPSTDGKVFCYALGIPILV 120  
 Qy 124 MFQSLGERINTLYRLHRAKGSLGMRAVDVSMANMYLIGFFSCISTICGAAAFSHYEH 183  
 Db 121 MFQSLGERINTLYRLHRAKGSLGMRAEVSMANMYLIGFFSCISTICGAAAFSYER 180  
 Qy 164 WTPFOAQTYCFCINLTIGFDTYALQKQALQTQPOVYAFSTFYVYLQGLTIGAFLNLYV 243  
 Db 181 WTPFOAQTYCFCITLTIGFDTYALQKQALQTQPOVYAFSTFYVYLQGLTIGAFLNLYV 240  
 Qy 244 LRFMTMNEDEKDAEHLALLTNGQACGGG-----GGSAHTTDASSTAA----- 291  
 Db 241 LRFMTMNEDEKDAEHLALLTNGQACGGG-----GGSAHTTDASSTAA----- 290  
 Qy 292 --GGGGFPRNNVAEVLHFSQMSMCISLWYKSRKLCYQSTIMIIIPRLSTSPTCVBOSHSSPGG 349  
 Db 301 GVGSGSPNNVAEVLHFSQMSMCISLWYKSRKLCYQSTIMIIIPRLSTSPTCVBOSHSSPGG 360  
 Qy 350 GFRYSQDTPSRRCLCSCGARSAAISSVSTLHSLSLSPRGMLKRSSV 394  
 Db 361 GGRYSQDTPSRRCLCSCGARSAAISSVSTLHSLSLAFRGMLKRSSV 405  
 Qy -  
 Db -  
 RESULT 9  
 AAU07620  
 XX AAU07620 standard; protein; 309 AA.  
 AC XX  
 XX ID AAB18807  
 ID AAB18807 standard; protein; 374 AA.  
 XX



Db	61 QLELVLIQSEPHRAGYQWKEFAGSFYFAITVITTIGYHAAPGTDAGKAFCMFYAVLGIPL	CC of diseases associated with altered KCNB activity or expression. Such diseases are cancer, heart disease, stroke, multiple sclerosis, Alzheimer's disease, Parkinson's disease, migraine, psychiatric disorders (such as depression, schizophrenia, bipolar diseases) and diseases related to the heart (such as arrhythmias), diseases related to pancreas (such as pancreatitis and diabetes).
QY	121 TLVMFQLSGLERMTNTLYRLIHLRAKKGLMERRADYVSMAANVYLIGFSCISTLCIGAAFSH 180	CC
Db	121 TLVMFQLSGLERMTNTYRLIHLRAKKGLMERRADYVSMAANVYLIGFSCISTLCIGAAFSQ 180	CC
QY	181 YEHWTFFQAYYYCFITLTIGFDVYALQDQALOTQPOQYAFSEVYILTGLTVIGAFLN 240	CC
Db	181 CEWWFFAHAYYYCFITLTIGFDVYALQDQALOTQPOQYAFSEVYILTGLTVIGAFLN 240	CC
QY	241 LVVLRFMTMNAEDEKDAEERALLTRNGQGGGGSAHTTDTASSTAAGGGCFRNVY 300	XX
Db	241 LVVLRFMTMNAEDEKDAEERALLTRNGQGGGGSAHTTDTASSTAAGGGCFRNVY 300	XX
QY	301 -AEVHFQSMCSCWYKRSREKLOSTPIMIIPRDLSSTDTCYBEOQSHSSPGGGGRYSDTPR 359.	XX
Db	301 -AEVHFQSMCSCWYKRSREKLOSTPIMIIPRDLSSTDTCYBEOQSHSSPGGGGRYSDTPR 359.	XX
QY	287 KADVPDLQSVCSTCYRSQD---YGRSRVAQNSPSAKLAPHYHSISYKIEEISPSTLK 343	XX
Db	287 KADVPDLQSVCSTCYRSQD---YGRSRVAQNSPSAKLAPHYHSISYKIEEISPSTLK 343	XX
QY	360 RCLCSGAPRPAISSVSTGLHSLSTRGLMKRRSSV 394	XX
Db	360 RCLCSGAPRPAISSVSTGLHSLSTRGLMKRRSSV 394	XX
Db	344 NSLFP---SPISSISPLGSFTDHQRLMKRRKSV 374	XX
<b>RESULT 1.2</b>		
ID	AAG63938 standard; protein; 374 AA.	AAE13279 standard; protein; 374 AA.
XX		XX
AC	AAG63938;	AAE13279;
XX		XX
DT	29-OCT-2001 (first entry)	12-FEB-2002 (first entry)
XX		
DE	Amino acid sequence of human potassium channel protein KCNB.	Human transporters and ion channels (TRICH)-6.
XX	Human: potassium channel protein; KCNB; breast tissue; cancer; stroke; potassium channel-associated disorder; brain associated disorder; epilepsy; Alzheimer's disease; Parkinson's disease; multiple sclerosis; migraine; psychiatric disorder; depression; schizophrenia; bipolar disease; heart disease; heart disease; arrhythmia; pancreatitis.	Human; transporter and ion channel; TRICH; akinesia; cystic fibrosis; diabetes mellitus; Parkinson's disease; myasthenia gravis; dementia; cardiac disorder; angina; hypertension; myocarditis; hyperglycaemia; neurological disorder; Alzheimer's disease; cataract; infertility; Wilson's disease; schizophrenia; Grave's disease; addison's disease; Huntington's disease; neuroprotective; menigitis; hypotensive; cardiotropic; neuroleptic; neuroprotective; neuroleptic; ophthalmological; antithyroid; anticonvulsant; goitre; antiinflammatory.
XX		
OS	Homo sapiens.	Homo sapiens.
PN	W0200166741-A2.	W0200166741-A2.
XX		
PD	13-SEP-2001.	AAE13279
XX		XX
PP	02-MAR-2001; 2001WD-US006801.	AAE13279;
XX		XX
PR	03-MAR-2000; 2000US-0166915P.	12-FEB-2002
XX		
PA	(TULSA-) TULARIK INC.	
XX		
P1	Mu D, Powers S;	FH
XX		Key
PP	WPI; 2001-522949/57.	FT
XX	N-NSDB; AAH74999.	Peptide
PR		FT
XX		Protein
PA	A nucleic acid encoding a potassium channel, termed KCNB (potassium channel 1 expressed in breast), useful in the diagnosis, prognosis or treatment of diseases associated with altered KCNB activity or expression, e.g. cancer and diabetes.	FT
XX		Domain
PS	Claim 16; Page 79; 82pp; English.	FT
XX		XX
CC	The present sequence represents a human potassium channel protein, termed KCNB. KCNB is expressed in breast tissue. The KCNB polypeptides are useful for identifying a compound that modulates its activity. The KCNB polypeptide and nucleic acid are useful for detecting cancer cells in biological samples. The inhibitor of the potassium channel polypeptide is useful for inhibiting proliferation of a cancer cell and for treating a potassium channel-associated disorder. The KCNB nucleic acids, proteins, and/or antibodies are useful in the diagnosis or prognosis, or treatment	Location/Qualifiers
CC		1..25
CC		/label= Signal_peptide
CC		26..374
CC		/note= "Human mature TRICH6 protein"
CC		225..243
CC		/label= Transmembrane_domain
CC		
PN	WO200177174-A2.	PN

XX	18-OCT-2001.	QY	301 -AEVLFQSMCSCLWYKSRKELQYSPIMLIPRLDLSITCVCQSHSSPGGGGRYSQDTSPR 359
XX	06-APR-2001; 2001WO-US011206.	Db	287 KADYPLQSVCSCTCYRSQD--YGGRSVAPQNSFAKLAPHFHSISYKIEEISPSPLIK 343
XX	06-APR-2000; 2000US-0195595P.	QY	360 RCLGSGAPRSAISSVSTGLHSLSTFRGLMKRRSSV 394
PR	12-APR-2000; 2000US-0196872P.	Db	344 NSLFP---SPISSPGHSFTDHQLMKRRSSV 374
PR	20-APR-2000; 2000US-0193020P.		
PR	28-APR-2000; 2000US-0200552P.		
PR	05-MAY-2000; 2000US-0202348P.		
PR	11-MAY-2000; 2000US-0203495P.		
XX	PA (INCY-) INCYTE GENOMICS INC.		
XX	Reddy R, Thornton M, Borowsky ML, Tang YT, Khan FA, Tribouley CM, Gandhi AR, Yao MG, Sadiqawala MS, Baughn MR, Nguyen DB, Polichy JL, Yue H, Seilhamer JJ, Walia NK, Lal P, Kearney L, Walsh RT, Lu DAM, Lu Y, Greene BD, Raumann BE, Patterson C;	WPI: 2002-017448/02.	RESULT 14
XX	N-PSDB; AAD21998.	XX	AAB22989 standard, protein; 374 AA.
XX	PT Peptides of human transporters and ion channels, useful for diagnosing, treating or preventing disorders of transport, neurological, muscle, immunological and cell proliferative disorders.	XX	ID AAB22989 standard, protein; 374 AA.
XX	PT Claim 1; Page 124-125; 150pp; English.	XX	XX
CC	The invention relates to human transporters and ion channels (TRICH) and the polynucleotides encoding them. The composition comprising TRICH or agonist of TRICH is useful for treating a disease or condition associated with decreased expression of functional TRICH or condition associated with overexpression of TRICH respectively. The composition comprising Ab is useful for diagnosing a condition of disease associated with expression of TRICH in a subject, where the disorders include a transport disorder such as akinines, cystic fibrosis, diabetes mellitus, Parkinson's disease, myasthenia gravis, cardiac disorders associated with transport e.g. angina hypertension, myocarditis, neurological disorders associated with transport e.g. Alzheimer's disease, Wilson's disease, schizophrenia, cataracts, inheritance, hyperglycaemia, Grave's disease, goitre, addison's disease, Huntington's disease, dementia, multiple sclerosis, bacterial and viral meningitis. TRICH DNA is useful for generating a transcript image of a tissue or cell type, which represents the global pattern of gene expression by a particular tissue or cell type. For analysing the proteome of a tissue or cell type. TRICH DNA is used in gene therapy. The present amino acid sequence is human TRICH5 protein	XX	XX
CC	Sequence 374 AA;	SQ	XX
CC	Query Match 54.7%; Score 1116; DB 5; Length 374; Best Local Similarity 59.0%; Pred. No. 3.5e-112; Matches 233; Conservative 44; Nsmatches 96; Indels 22; Gaps 5;	QY	1. MKRNQVRTLALIVCFPTYLIVGAAVFDALLESEPELIERQDLERQELARYNUSQGGVB 60
CC		Db	1. MKRNQVRTLALIVCFPTYLIVGAAVFDALLESEPELIERQDLERQELARYNUSQGGVB 60
CC		QY	61 ELERVYVLRKPHKAGYQWRFQASPEFYFAITVTTIGYGHAAPISTDGKVFMVYALLGIPL 120
CC		Db	61 QLELVYLQSERPTVRYQWKFQASPEFYFAITVTTIGYGHAAPISTDGKVFMVYAVLGIPL 120
CC		QY	121 TLVMSQSLGERMNTFTRYLLKRIKCCGMRNTDVSMENATVGFSCMGULCIGAAAFSQ 180
CC		Db	121 TLVMSQSLGERMNTFTRYLLKRIKCCGMRNTDVSMENATVGFSCMGULCIGAAAFSQ 180
CC		QY	181 YEHWTFFQAYYCFTLTIGFQDYLVALQDKOALOTQPOVAFSFWYVILTGLTVIGAFLN 240
CC		Db	181 CBEWSFPHAYYCFTLTIGFQDYLVALQTKGALQRKPLXVAFSMVILVGLTVIGAFLN 240
CC		QY	241 LVVLRPMTMNAEDEKRDAEHRALLTRNGQAGGGGGGSIAHTTDASSTAAGGGGFRNTV 300
CC		Db	241 LVVLRPMTMNAEDEKRDAEHRALLTRNGQAGGGGGGSIAHTTDASSTAAGGGGFRNTV 300
CC		QY	241 LVVLRPMTMNAEDEKRDAEHRALLTRNGQAGGGGGGSIAHTTDASSTAAGGGGFRNTV 300
CC		Db	241 LVVLRPMTMNAEDEKRDAEHRALLTRNGQAGGGGGGSIAHTTDASSTAAGGGGFRNTV 300



CC TWIK-8, IC47611, IC47615, HNMDA-1, TWIK-9, alpha-2delta-4, 54414 and  
 CC 53763 ICF nucleic acids and proteins may be used for preventing,  
 CC diagnosing and treating ICF-related diseases. The sequences may be used  
 CC to treat disorders associated with decreased expression by rectifying  
 CC mutations or deletions in a patient's genome that affect the activity of  
 CC ICF proteins by expressing inactive proteins or to supplement the  
 CC patients own production of ICF proteins. The proteins may also be used as  
 CC antigens in the production of antibodies against ICF proteins and in  
 CC assays to identify modulators of ICF protein expression and activity. The  
 CC anti-ICF protein antibodies, agonists and antagonists may be used to  
 CC regulate ICF protein expression and activity. The antibodies may also be  
 CC used as diagnostic agents for detecting the presence of ICF proteins in  
 CC samples (e.g. by immunoassay). The nucleic acids and proteins may be used  
 CC to prevent, diagnose and treat a wide variety of disorders, e.g. cancers  
 CC and leukaemia; Alzheimer's disease, Parkinson's disease, multiple  
 CC sclerosis, epilepsy, hepatic disorders and cardiovascular disorders. This  
 CC sequence represents the human TWIK-9 protein of the invention. Note: The  
 CC sequence data for this patent is also available in electronic format from  
 CC USPTO at seqdata.uspto.gov/sequence.html.

SQ Sequence 374 AA:

Query	Match	Score	Length
Qy	1 MKRQNYPTALIIVCTETYLGVAAVEDALESPPELIERORLRLRQEFLRARNYLSSGGYE 60	54.7%	374;
Db	1 MKRQNYRTLSLVCTFTYLLGRAVEFALKAEERIGKYNISSEDYR 60	59.0%	DB 8;
Qy	61 ELERVVLRLKEPKAGIQMRRPASPFYAFITVTITIGHAAPSTDGKVPCMFYALLGPL 120	59.0%	Length 374;
Db	61 QLEFLVILQSEPRAGQWKEAGSFYAFITVTITIGHAAPSTDGKVPCMFYAVIGPL 120	59.0%	Pred. No. 3.5e-112;
Qy	121 TLVMFQSIGERINTLVRLHRAKKKGMRADVSANMVLIQFFFSCTISTLIGABAASH 180	59.0%	Mismatches 44;
Db	121 TLVMFQSIGERINTLVRLHRAKKKGMRNTDVSMEMNTVMTGFFSGMTCIGAAAFSQ 180	59.0%	Indels 22;
Qy	181 YEHWTFFQQAYYYCFCITLTIGFSDYVAQKQDQLCQYAFSFLVYLQGTVGAFLN 240	59.0%	Gaps 5;
Db	181 CSEWSFFPAAYYCFCITLTIGFSDYVAQKQDQLCQYAFSFLVYLQGTVGAFLN 240	59.0%	
Qy	241 LVVLFRENTMNAEDEKRDMEHRLTRNGQAGGGGGSAHTTDAGSTAAGGGFRNVT 300	59.0%	
Db	241 LVVLFRENTMNEEDERRDABERASL----AGNRSNSVTHIPEEPRES-----RPRY 286	59.0%	
Qy	301 -AEVLHFOSMCSCSLWYKSRKQYSIPNIPPDLSSTDTCYEQSHSSPPGGGGRYSIDTPSR 359	59.0%	
Db	301 -AEVLHFOSMCSCSLWYKSRKQYSIPNIPPDLSSTDTCYEQSHSSPPGGGGRYSIDTPSR 359	59.0%	
Qy	344 NSLFP---SPISSISPLHSFTDHQRLMKRRXSV 374	59.0%	
Db	344 NSLFP---SPISSISPLHSFTDHQRLMKRRXSV 374	59.0%	

Search completed: July 13, 2005, 08:39:50  
 Job time : 100.204 sec

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OM protein - protein search, using sw model

Run on: July 13, 2005, 08:02:40 ; Search time 20.7368 Seconds  
(without alignments)  
1828.118 Million cell updates/sec

Title: US-09-503-089A-5  
Perfect score: 2042  
Sequence: 1 MKRQNVRLALIVCTFTYLL.....STGLHSLSTERGLMKRRSSV 394

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing First 45 summaries

Database : PIR\_79;\*  
1: p1r1;\*  
2: p1r2;\*  
3: p1r3;\*  
4: p1r4;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Description
		%	Length DB ID
1	846	41.4	TASK-5 Protein - h
	820	40.2	probable potassium outward rectifier
3	806.5	39.5	hypothetical prote
4	599	29.3	probable potassium inward rectifier P
6	320.5	15.7	hypothetical prote
7	307.5	15.1	protein T12C9.3 [i]
8	276.5	14.3	hypothetical prote
9	275	13.5	hypothetical prote
11	269	13.1	hypothetical prote
12	262	12.8	hypothetical prote
13	261.5	12.8	hypothetical prote
14	259.5	12.7	hypothetical prote
15	258	12.6	hypothetical prote
16	255	12.6	hypothetical prote
17	255.1	12.6	hypothetical prote
18	251	12.3	potassium channel
19	251	12.3	potassium channel
20	250	12.2	probable potassium channel
21	248	12.1	hypothetical prote
22	247.5	12.1	hypothetical prote
23	245	12.0	hypothetical prote
24	244	11.9	potassium channel
25	243	11.9	hypothetical prote
26	239.5	11.7	hypothetical prote
27	235.5	11.5	hypothetical prote
28	234.5	11.5	hypothetical prote
29	231.5	11.3	probable potassium channel
30	231.5	11.3	hypothetical prote
31	229	11.2	hypothetical prote
32	229	11.2	hypothetical prote
33	222.5	10.9	hypothetical prote
34	216	10.6	hypothetical prote
35	215.5	10.6	hypothetical prote
36	211	10.3	hypothetical prote
37	210.5	10.3	hypothetical prote
38	210	10.3	hypothetical prote
39	205.5	10.1	hypothetical prote
40	201.5	9.9	hypothetical prote
41	201.5	9.9	hypothetical prote
42	200.5	9.8	hypothetical prote
43	199.5	9.8	hypothetical prote
44	193.5	9.5	hypothetical prote
45	190.5	9.3	hypothetical prote

## ALIGNMENTS

RESULT 1									
JC7703	Task-5 Protein - human	C;Species: Homo sapiens (man)	C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001	R;Kim, D.; Gnatenko, C.	Biochem. Biophys. Res. Commun. 284, 923-930, 2001	A;Title TASK-5, a new member of the tandem-pore K+ channel family.	A;Reference number: JC7703 ; PMID:21303050 ; PMID:11409881	A;Molecule type: DNA	A;Residues: 1-330 <KIN>
									A;Cross-references: GB:AL118522
									C;Comment: This protein, a new member of the tandem-pore K+ channel family, secretes hormone secretion, but does not produce a functional plasma membrane K+ current by its C;Genetics:
									A;Gene: task-5
									A;Map position: 20q12
									C;Keywords: transmembrane protein
					F;7-30/Domain: transmembrane segment #status predicted <TMS1>				F;107-128/Domain: transmembrane segment #status predicted <TMS2>
					F;129-155/Region: hydrophobic cytoplasmic linker #status predicted				F;156-180/Domain: transmembrane segment #status predicted <TMS3>
					F;220-240/Domain: transmembrane segment #status predicted <TMS4>				Query Match 41.4%; Score 846; DB 2; Length 330;
					Best Local Similarity 64.7%; Prod. No. 1e-68; Matches 167; Conservative 32; Mismatches 59; Indels 0; Gaps 0;				Matches 61 ELRVVRLKPHKAQVWRFASFSYFAITVTTIGYCHAAPSTDGGKVFCMFYALLGIPL 120
					Qy 1 MGRQNTVTLAVTCFTYLLGVAFDALESEBLIBQRLEQRQEFLARYNSQGGYTS 60				Db 1 MRPSVRAGLVLTCLCYLVGVAFDALESESGRQLLYQKGARRKFGESADYR 60
					Qy 2 :   :				

RESULT 2

T43509  
Prokaryotic potassium channel chain n2P38 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 09-Jul-2004  
C;Accession: T43509  
R;Wang, Z.W.; Salkoff, L.  
Submitted to the EMBL Data Library, August 1998  
A;Description: Potassium channels in C. elegans.  
A;Accession: T42450  
A;Status: preliminary; translated from GB/EMBL/DDJB  
A;Molecule type: mRNA  
A;Residues: 1-329 <WAN>  
A;Cross-references: UNIPROT:O17185; EMBL:AF083652; PIDN: AAC32863.1

Query Match 40.2%; Score 820; DB 2; Length 329;  
Best Local Similarity 48.3%; Pred. No. 2.2e-66;  
Matches 172; Conservative 54; Mismatches 84; Indels 46; Gaps 7;

Qy 1 MRQNVTPLALIVCTFTYLLGRAVEDALESSPELTERQRLELRQBLARYNLNSQGYE 60  
Db 1 MRQNIRTLISLIVCTLYLLGRAVEDALETENELQRKLVQRREKLIKTYNNMSNADYE 60  
Qy 61 ELERVVRLRKPAGVQWRPAGSFYPAITVTTIGYCHAAPSTDGGKVFCMFYALIGIPL 120  
Db 61 ILEATIVRSVPKRAGVQWKSFAGYPAITVTTIGYCHAAPSTDGGKVFCMFYALAGIPL 120

RESULT 4  
T19860  
hypothetical protein C40C9.1 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000  
C;Accession: T19860  
R;Hembry, C.  
Submitted to the EMBL Data Library, March 1996  
A;Reference number: Z19188  
A;Accession: T19860  
A;Status: preliminary; translated from GB/EMBL/DDJB  
A;Molecule type: DNA  
A;Residues: 1-34 <WIL>  
A;Cross-references: EMBL:Z70266; PIDN: CRA94204.1; GSPDB: GN00028; CESSP: C40C9.1  
A;Experimental source: clone C40C9  
A;Genetics:  
A;Map position: X  
A;Introns: 34/1; 60/2; 98/1; 145/3; 160/3; 181/1; 204/1; 252/2; 279/2; 306/3

Query Match 29.3%; Score 599; DB 2; Length 334;  
Best Local Similarity 46.1%; Pred. No. 2.2e-46;  
Matches 119; Conservative 46; Mismatches 81; Indels 12; Gaps 3;

Qy 4 QNVRTALIVCTFTYLLVGADEVALESEPELIERORLERRQEETARYNLSQG3YEELE 63  
Db 7 KSARALLLILSTFTVLLFGAMVFDKLESEKDWTWREDEIERITDRJHKYNFSERDHLFEE 66

Qy 239 LNLLVVRMFTMNAEDEKRDAEHRL---LTNGQAGGGGSAHTTDTASSTAAGGG 294  
Db 238 MNLLVVRFLMTNEDBRDQEAIALLAAGLVRVGDPPTADDDEGRLPLSDNVSLAS--- 292

Qy 295 GFRNVAEVHLHQSMCSCLWYSREKLQYISPMIIPRDLSITSDTCVBEQSHSSPGGG 350  
Db 293 -----GSC-YQLPDEKLHR-----HRKTEBPHGG 316

RESULT 3  
T32347  
outward rectifier potassium channel homolog twk-23 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T32347  
R;Murray, J.; Wohldmann, P.-i. O'Neal, D.  
Submitted to the EMBL Data Library, September 1997  
A;Description: The sequence of C. elegans cosmid F34D6.  
A;Accession: T32347  
A;Status: preliminary; translated from GB/EMBL/DDJB  
A;Molecule type: DNA  
A;Residues: 1-336 <WDR>  
A;Cross-references: UNIPROT:O17185; EMBL:AF025454; PIDN: AAC71151.1; GSPDB: GN00020; CESSP:  
A;Experimental source: strain Bristol N2; clone F34D6  
C;Genetics:  
A;Gene: twk-23; CESP: F34D6.3  
A;Map position: 2  
A;Introns: 44/3; 102/1; 136/1; 180/1; 207/1; 265/2; 296/3

Query Match 39.5%; Score 806.5; DB 2; Length 336;  
Best Local Similarity 47.4%; Pred. No. 3.8e-65;  
Matches 172; Conservative 54; Mismatches 84; Indels 53; Gaps 8;

Qy 1 MRQNVTPLALIVCTFTYLLGRAVEDALESSPELTERQRLELRQBLARYNLNSQGYE 53  
Db 1 MRQNIRTLISLIVCTLYLLGRAVEDALETENELQRKLVQRREKLIKTYNN 60

RESULT 5  
T43361  
probable potassium channel chain n2P20 - Caenorhabditis elegans



A;Accession: T25392	Qy	119 PLTLYMFQSLSGERINTLVRVLLHARKG-----LGMRADVS 155
A;Preliminary; translated from GB/EMBL/DDJB	Db	369 PIAITIGDQKFLSECTIWLKARWKGSARLDMSWKRFRGLESDISDLESASNQNQDS 428
A;Molecule type: DNA		
A;Residues: 1-393 <WIL>		
A;Cross-references: UNIPROT:Q9XU07; EMBL:Z92813; PIDN:CAB07286.1; CESP:T2	Qy	156 MANM-----VLIGFFSC1STLICGAAAFSHYEHNTFFQQAYYCPITLTIGFD 204
A;Experimental source: clone T28A8	Db	429 ILDMMDDEIDKSEEVPMVFTILLYIAFGCILFSLTDWSYMDAFYSFISLTIGFD 488
C;Genetics:		
A;Gene: CESP:T28A8.1		
A;Map Position: 3	Qy	205 YVALQDQALQTQPVQVAFSEVYILITGLTVGAFNLNUVLFM 247
A;Intron: 73/1; 112/3; 179/2; 209/3; 287/2; 310/3; 364/2	Db	489 IVPENHD-----YIAIMLIVGSLSYTTMCIDLAGIQYI 523
Query Match		RESULT 10
Best Local Similarity 26.6%; Pred. No. 1.4e-18;		T23907
Matches 78; Conservative 57; Mismatches 96; Indels 62; Gaps 9;		
		hypothetical protein R04F11.4 - Caenorhabditis elegans
		C;Species: Caenorhabditis elegans
		C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
		R:Harris B.
		submitted to the EMBL Data Library, June 1996
		A;Reference number: Z19816
		A;Accession: T23907
		A;Status: preliminary; translated from GB/EMBL/DDBJ
		A;Molecule type: DNA
		A;Residues: 1-524 <WIL>
		A;Cross-references: UNIPROT:Q21729; EMBL:Z74475; PIDN:CAA99957.1; CESP:GN00023; CESP:RC
		A;Experimental source: clone R04F11
		C;Genetics:
		A;Gene: CESP:R04F11.4
		A;Map position: 5
		A;Intron: 35/3; 83/2; 131/1; 170/1; 261/1; 306/1; 338/1; 369/1; 489/2
		Query Match 13.5%; Score 275; DB 2; Length 524;
		Best Local Similarity 23.9%; Pred. No. 8.2e-17;
		Matches 88; Conservative 38; Mismatches 92; Indels 150; Gaps 9;
		Query 11 LIVCTFTYLGVAAVEDALESEPELIERQRQLERLQELRLARY-----52
		Db 18 LVLLSGTYLIGALCHHYKPYEQQLRNETSRRGELKXRVMDQLWRMSNNNTAYSTWR 77
		Query 53 NLSQGGYYEELEERYVVL-----RLKPH-----KAGTQWRFAGSFYPAITVTTIGGHAP 101
		Db 78 QTANQMDMLLRDVWDYDTNMYTPDVIYGDPKIKWSPNSFISFWNTWAITTGGHVIP 137
		Query 102 STDGSKVFCMPYALLGIPITLVMPQSGLERINTLV-----
		Db 138 RTDGEVALLYALGIPILPLVLTADIGRFLATYIKLHHGYMAVMSFVINSCLCKICIA 197
		Query 137 -----RY-----LLRAKK-----GIGMR-----150
		Db 198 CCWIRLPRRRHTPMPTELLQRTQKLYPNNNNPNPTVATAASAGGGTGRRKQQRDNVDAG 257
		Query 151 -----RADVSMANVVLIGFFCISTLICIG-----
		Db 258 TFDN12BNDSEGGGENEGESEEQ1QFDPSENHEKRVSVLFILLIMLGY-----VAGM 311
		Query 175 AAFAFSHYEHNTFFQQAYYCPITLTIGFDYVALQDQALQTQPVQVAFSEVYILITGLTV 234
		hypothetical protein F20a1.7 - Caenorhabditis elegans
		C;Species: Caenorhabditis elegans
		C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
		C;Accession: T30037
RESULT 9		Query Match 13.5%; Score 276.5; DB 2; Length 1910;
protein r12c9.3 [imported] - Caenorhabditis elegans		Best Local Similarity 23.3%; Pred. No. 2.9e-16;
C;Species: Caenorhabditis elegans		Mismatches 80; Conservative 49; Mismatches 107; Indels 107; Gaps 8;
C;Accession: H88124	Qy	Db 312 AYIVRMWEENTFEAFYFCFVTVTIGFDIVPANYD-----WLPATLAYIVFGLII 363
R;Anonymous: The C. elegans Sequencing Consortium.		Query 235 IGAFINLV 242
Science 282, 2012-2018, 1998		Db 364 TTMCIDLV 371
A;Title: Genome sequence of the nematode <i>C. elegans</i> : a platform for investigating biology		Query 249 INNEKEYWKEDIEKEMLHYSEKLYKAFAKEQVTRYSVDTRTIGFEGSSYSEADETGDSE 308
A;Reference number: A750000; MUID:99069613; PMID:9851916		Db 68 RLKPHKAG-----VQWRFAGSFYPAITVTTIGYGAAPSTDGKVFCMPYALLGI 118
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/projects/C_elegans/		Db 309 RKRHRHAKNRKGDRGSEWMTSSALPAATTMATICGNTVPTPIGLRACVLFAFGA 368
A;Accession: H88124		Query 4 ONVRTLA-----LIVCTFTYLGVAAVDALES--EPELLERORQELRLQELRLARY 53
A;Status: preliminary		Db 169 QNTRKYANALPHIVLVCVCIYATGAWIFTLESPENDRIKETGRKTIAEMRSNLIXK 248
A;Molecule type: DNA		Query 54 LS-----QGGEYEELEERV--VL 67
A;Residues: 1-1910 <STO>		Db 249 INNEKEYWKEDIEKEMLHYSEKLYKAFAKEQVTRYSVDTRTIGFEGSSYSEADETGDSE 308
A;Cross-references: GB:chr_II; PIDN:AC71141.1; PID:91086770; GSPDB:GN00020; CESP:T12C9.3	Qy	Query 249 INNEKEYWKEDIEKEMLHYSEKLYKAFAKEQVTRYSVDTRTIGFEGSSYSEADETGDSE 308
C;Genetics:		Db 68 RLKPHKAG-----VQWRFAGSFYPAITVTTIGYGAAPSTDGKVFCMPYALLGI 118
A;Gene: T12c9.3		Db 309 RKRHRHAKNRKGDRGSEWMTSSALPAATTMATICGNTVPTPIGLRACVLFAFGA 368
A;Map position: 2		Query 249 INNEKEYWKEDIEKEMLHYSEKLYKAFAKEQVTRYSVDTRTIGFEGSSYSEADETGDSE 308
Query Match 13.5%; Score 276.5; DB 2; Length 1910;		Db 68 RLKPHKAG-----VQWRFAGSFYPAITVTTIGYGAAPSTDGKVFCMPYALLGI 118
Best Local Similarity 23.3%; Pred. No. 2.9e-16;		Db 309 RKRHRHAKNRKGDRGSEWMTSSALPAATTMATICGNTVPTPIGLRACVLFAFGA 368
Mismatches 80; Conservative 49; Mismatches 107; Indels 107; Gaps 8;		Query 249 INNEKEYWKEDIEKEMLHYSEKLYKAFAKEQVTRYSVDTRTIGFEGSSYSEADETGDSE 308
		Db 68 RLKPHKAG-----VQWRFAGSFYPAITVTTIGYGAAPSTDGKVFCMPYALLGI 118
		Db 309 RKRHRHAKNRKGDRGSEWMTSSALPAATTMATICGNTVPTPIGLRACVLFAFGA 368
		Query 249 INNEKEYWKEDIEKEMLHYSEKLYKAFAKEQVTRYSVDTRTIGFEGSSYSEADETGDSE 308
		Db 68 RLKPHKAG-----VQWRFAGSFYPAITVTTIGYGAAPSTDGKVFCMPYALLGI 118
		Db 309 RKRHRHAKNRKGDRGSEWMTSSALPAATTMATICGNTVPTPIGLRACVLFAFGA 368
		Query 249 INNEKEYWKEDIEKEMLHYSEKLYKAFAKEQVTRYSVDTRTIGFEGSSYSEADETGDSE 308
		Db 68 RLKPHKAG-----VQWRFAGSFYPAITVTTIGYGAAPSTDGKVFCMPYALLGI 118
		Db 309 RKRHRHAKNRKGDRGSEWMTSSALPAATTMATICGNTVPTPIGLRACVLFAFGA 368
		Query 249 INNEKEYWKEDIEKEMLHYSEKLYKAFAKEQVTRYSVDTRTIGFEGSSYSEADETGDSE 308
		Db 68 RLKPHKAG-----VQWRFAGSFYPAITVTTIGYGAAPSTDGKVFCMPYALLGI 118
		Db 309 RKRHRHAKNRKGDRGSEWMTSSALPAATTMATICGNTVPTPIGLRACVLFAFGA 368
		Query 249 INNEKEYWKEDIEKEMLHYSEKLYKAFAKEQVTRYSVDTRTIGFEGSSYSEADETGDSE 308
		Db 68 RLKPHKAG-----VQWRFAGSFYPAITVTTIGYGAAPSTDGKVFCMPYALLGI 118
		Db 309 RKRHRHAKNRKGDRGSEWMTSSALPAATTMATICGNTVPTPIGLRACVLFAFGA 368
		Query 249 INNEKEYWKEDIEKEMLHYSEKLYKAFAKEQVTRYSVDTRTIGFEGSSYSEADETGDSE 308
		Db 68 RLKPHKAG-----VQWRFAGSFYPAITVTTIGYGAAPSTDGKVFCMPYALLGI 118
		Db 309 RKRHRHAKNRKGDRGSEWMTSSALPAATTMATICGNTVPTPIGLRACVLFAFGA 368
		Query 249 INNEKEYWKEDIEKEMLHYSEKLYKAFAKEQVTRYSVDTRTIGFEGSSYSEADETGDSE 308
		Db 68 RLKPHKAG-----VQWRFAGSFYPAITVTTIGYGAAPSTDGKVFCMPYALLGI 118
		Db 309 RKRHRHAKNRKGDRGSEWMTSSALPAATTMATICGNTVPTPIGLRACVLFAFGA 368
		Query 249 INNEKEYWKEDIEKEMLHYSEKLYKAFAKEQVTRYSVDTRTIGFEGSSYSEADETGDSE 308
		Db 68 RLKPHKAG-----VQWRFAGSFYPAITVTTIGYGAAPSTDGKVFCMPYALLGI 118
		Db 309 RKRHRHAKNRKGDRGSEWMTSSALPAATTMATICGNTVPTPIGLRACVLFAFGA 368
		Query 249 INNEKEYWKEDIEKEMLHYSEKLYKAFAKEQVTRYSVDTRTIGFEGSSYSEADETGDSE 308
		Db 68 RLKPHKAG-----VQWRFAGSFYPAITVTTIGYGAAPSTDGKVFCMPYALLGI 118
		Db 309 RKRHRHAKNRKGDRGSEWMTSSALPAATTMATICGNTVPTPIGLRACVLFAFGA 368
		Query 249 INNEKEYWKEDIEKEMLHYSEKLYKAFAKEQVTRYSVDTRTIGFEGSSYSEADETGDSE 308
		Db 68 RLKPHKAG-----VQWRFAGSFYPAITVTTIGYGAAPSTDGKVFCMPYALLGI 118
		Db 309 RKRHRHAKNRKGDRGSEWMTSSALPAATTMATICGNTVPTPIGLRACVLFAFGA 368
		Query 249 INNEKEYWKEDIEKEMLHYSEKLYKAFAKEQVTRYSVDTRTIGFEGSSYSEADETGDSE 308
		Db 68 RLKPHKAG-----VQWRFAGSFYPAITVTTIGYGAAPSTDGKVFCMPYALLGI 118
		Db 309 RKRHRHAKNRKGDRGSEWMTSSALPAATTMATICGNTVPTPIGLRACVLFAFGA 368
		Query 249 INNEKEYWKEDIEKEMLHYSEKLYKAFAKEQVTRYSVDTRTIGFEGSSYSEADETGDSE 308
		Db 68 RLKPHKAG-----VQWRFAGSFYPAITVTTIGYGAAPSTDGKVFCMPYALLGI 118
		Db 309 RKRHRHAKNRKGDRGSEWMTSSALPAATTMATICGNTVPTPIGLRACVLFAFGA 368
		Query 249 INNEKEYWKEDIEKEMLHYSEKLYKAFAKEQVTRYSVDTRTIGFEGSSYSEADETGDSE 308
		Db 68 RLKPHKAG-----VQWRFAGSFYPAITVTTIGYGAAPSTDGKVFCMPYALLGI 118
		Db 309 RKRHRHAKNRKGDRGSEWMTSSALPAATTMATICGNTVPTPIGLRACVLFAFGA 368
		Query 249 INNEKEYWKEDIEKEMLHYSEKLYKAFAKEQVTRYSVDTRTIGFEGSSYSEADETGDSE 308
		Db 68 RLKPHKAG-----VQWRFAGSFYPAITVTTIGYGAAPSTDGKVFCMPYALLGI 118
		Db 309 RKRHRHAKNRKGDRGSEWMTSSALPAATTMATICGNTVPTPIGLRACVLFAFGA 368
		Query 249 INNEKEYWKEDIEKEMLHYSEKLYKAFAKEQVTRYSVDTRTIGFEGSSYSEADETGDSE 308
		Db 68 RLKPHKAG-----VQWRFAGSFYPAITVTTIGYGAAPSTDGKVFCMPYALLGI 118
		Db 309 RKRHRHAKNRKGDRGSEWMTSSALPAATTMATICGNTVPTPIGLRACVLFAFGA 368
		Query 249 INNEKEYWKEDIEKEMLHYSEKLYKAFAKEQVTRYSVDTRTIGFEGSSYSEADETGDSE 308
		Db 68 RLKPHKAG-----VQWRFAGSFYPAITVTTIGYGAAPSTDGKVFCMPYALLGI 118
		Db 309 RKRHRHAKNRKGDRGSEWMTSSALPAATTMATICGNTVPTPIGLRACVLFAFGA 368
		Query 249 INNEKEYWKEDIEKEMLHYSEKLYKAFAKEQVTRYSVDTRTIGFEGSSYSEADETGDSE 308
		Db 68 RLKPHKAG-----VQWRFAGSFYPAITVTTIGYGAAPSTDGKVFCMPYALLGI 118
		Db 309 RKRHRHAKNRKGDRGSEWMTSSALPAATTMATICGNTVPTPIGLRACVLFAFGA 368
		Query 249 INNEKEYWKEDIEKEMLHYSEKLYKAFAKEQVTRYSVDTRTIGFEGSSYSEADETGDSE 308
		Db 68 RLKPHKAG-----VQWRFAGSFYPAITVTTIGYGAAPSTDGKVFCMPYALLGI 118
		Db 309 RKRHRHAKNRKGDRGSEWMTSSALPAATTMATICGNTVPTPIGLRACVLFAFGA 368
		Query 249 INNEKEYWKEDIEKEMLHYSEKLYKAFAKEQVTRYSVDTRTIGFEGSSYSEADETGDSE 308
		Db 68 RLKPHKAG-----VQWRFAGSFYPAITVTTIGYGAAPSTDGKVFCMPYALLGI 118
		Db 309 RKRHRHAKNRKGDRGSEWMTSSALPAATTMATICGNTVPTPIGLRACVLFAFGA 368
		Query 249 INNEKEYWKEDIEKEMLHYSEKLYKAFAKEQVTRYSVDTRTIGFEGSSYSEADETGDSE 308
		Db 68 RLKPHKAG-----VQWRFAGSFYPAITVTTIGYGAAPSTDGKVFCMPYALLGI 118
		Db 309 RKRHRHAKNRKGDRGSEWMTSSALPAATTMATICGNTVPTPIGLRACVLFAFGA 368
		Query 249 INNEKEYWKEDIEKEMLHYSEKLYKAFAKEQVTRYSVDTRTIGFEGSSYSEADETGDSE 308
		Db 68 RLKPHKAG-----VQWRFAGSFYPAITVTTIGYGAAPSTDGKVFCMPYALLGI 118
		Db 309 RKRHRHAKNRKGDRGSEWMTSSALPAATTMATICGNTVPTPIGLRACVLFAFGA 368
		Query 249 INNEKEYWKEDIEKEMLHYSEKLYKAFAKEQVTRYSVDTRTIGFEGSSYSEADETGDSE 308
		Db 68 RLKPHKAG-----VQWRFAGSFYPAITVTTIGYGAAPSTDGKVFCMPYALLGI 118
		Db 309 RKRHRHAKNRKGDRGSEWMTSSALPAATTMATICGNTVPTPIGLRACVLFAFGA 368
		Query 249 INNEKEYWKEDIEKEMLHYSEKLYKAFAKEQVTRYSVDTRTIGFEGSSYSEADETGDSE 308
		Db 68 RLKPHKAG-----VQWRFAGSFYPAITVTTIGYGAAPSTDGKVFCMPYALLGI 118
		Db 309 RKRHRHAKNRKGDRGSEWMTSSALPAATTMATICGNTVPTPIGLRACVLFAFGA 368
		Query 249 INNEKEYWKEDIEKEMLHYSEKLYKAFAKEQVTRYSVDTRTIGFEGSSYSEADETGDSE 308
		Db 68 RLKPHKAG-----VQWRFAGSFYPAITVTTIGYGAAPSTDGKVFCMPYALLGI 118
		Db 309 RKRHRHAKNRKGDRGSEWMTSSALPAATTMATICGNTVPTPIGLRACVLFAFGA 368
		Query 249 INNEKEYWKEDIEKEMLHYSEKLYKAFAKEQVTRYSVDTRTIGFEGSSYSEADETGDSE 308
		Db 68 RLKPHKAG-----VQWRFAGSFYPAITVTTIGYGAAPSTDGKVFCMPYALLGI 118
		Db 309 RKRHRHAKNRKGDRGSEWMTSSALPAATTMATICGNTVPTPIGLRACVLFAFGA 368
		Query 249 INNEKEYWKEDIEKEMLHYSEKLYKAFAKEQVTRYSVDTRTIGFEGSSYSEADETGDSE 308
		Db 68 RLKPHKAG-----VQWRFAGSFYPAITVTTIGYGAAPSTDGKVFCMPYALLGI 118
		Db 309 RKRHRHAKNRKGDRGSEWMTSSALPAATTMATICGNTVPTPIGLRACVLFAFGA 368
		Query 249 INNEKEYWKEDIEKEMLHYSEKLYKAFAKEQVTRYSVDTRTIGFEGSSYSEADETGDSE 308
		Db 68 RLKPHKAG-----VQWRFAGSFYPAITVTTIGYGAAPSTDGKVFCMPYALLGI 118
		Db 309 RKRHRHAKNRKGDRGSEWMTSSALPAATTMATICGNTVPTPIGLRACVLFAFGA 368
		Query 249 INNEKEYWKEDIEKEMLHYSEKLYKAFAKEQVTRYSVDTRTIGFEGSSYSEADETGDSE 308
		Db 68 RLKPHKAG-----VQWRFAGSFYPAITVTTIGYGAAPSTDGKVFCMPYALLGI 118
		Db 309 RKRHRHAKNRKGDRGSEWMTSSALPAATTMATICGNTVPTPIGLRACVLFAFGA 368
		Query 249 INNEKEYWKEDIEKEMLHYSEKLYKAFAKEQVTRYSVDTRTIGFEGSSYSEADETGDSE 308
		Db 68 RLKPHKAG-----VQWRFAGSFYPAITVTTIGYGAAPSTDGKVFCMPYALLGI 118
		Db 309 RKRHRHAKNRKGDRGSEWMTSSALPAATTMATICGNTVPTPIGLRACVLFAFGA 368
		Query 249 INNEKEYWKEDIEKEMLHYSEKLYKAFAKEQVTRYSVDTRTIGFEGSSYSEADETGDSE 308
		Db 68 RLKPHKAG-----VQWRFAGSFYPAITVTTIGYGAAPSTDGKVFCMPYALLGI 118
		Db 309 RKRHRHAKNRKGDRGSEWMTSSALPAATTMATICGNTVPTPIGLRACVLFAFGA 368
		Query 249 INNEKEYWKEDIEKEMLHYSEKLYKAFAKEQVTRYSVDTRTIGFEGSSYSEADETGDSE 308
		Db 68 RLKPHKAG-----VQWRFAGSFYPAITVTTIGYGAAPSTDGKVFCMPYALLGI 118
		Db 309 RKRHRHAKNRKGDRGSEWMTSSALPAATTMATICGNTVPTPIGLRACVLFAFGA 368
		Query 249 INNEKEYWKEDIEKEMLHYSEKLYKAFAKEQVTRYSVDTRTIGFEGSSYSEADETGDSE 308
		Db 68 RLKPHKAG-----VQWRFAGSFYPAITVTTIGYGAAPSTDGKVFCMPYALLGI 118
		Db 309 RKRHRHAKNRKGDRGSEWMTSSALPAATTMATICGNTVPTPIGLRACVLFAFGA 368
		Query 249 INNEKEYWKEDIEKEMLHYSEKLYKAFAKEQVTRYSVDTRTIGFEGSSYSEADETGDSE 308
		Db 68 RLKPHKAG-----VQWRFAGSFYPAITVTTIGYGAAPSTDGKVFCMPYALLGI 118
		Db 309 RKRHRHAKNRKGDRGSEWMTSSALPAATTMATICGNTVPTPIGLRACVLFAFGA 368
		Query 249 INNEKEYWKEDIEKEMLHYSEKLYKAFAKEQVTRYSVDTRTIGFEGSSYSEADETGDSE 308
		Db 68 RLKPHKAG-----VQWRFAGSFYPAITVTTIGYGAAPSTDGKVFCMPYALLGI 118
		Db 309 RKRHRHAKNRKGDRGSEWMTSSALPAATTMATICGNTVPTPIGLRACVLFAFGA 368
		Query 249 INNEKEYWKEDIEKEMLHYSEKLYKAFAKEQVTRYSVDTRTIGFEGSSYSEADETGDSE 308
		Db 68 RLKPHKAG-----VQWRFAGSFYPAITVTTIGYGAAPSTDGKVFCMPYALLGI 118
		Db 309 RKRHRHAKNRKGDRGSEWMTSSALPAATTMATICGNTVPTPIGLRACVLFAFGA 368
		Query 249 INNEKEYWKEDIEKEMLHYSEKLYKAFAKEQVTRYSVDTRTIGFEGSSYSEADETGDSE 308
		Db 68 RLKPHKAG-----VQWRFAGSFYPAITVTTIGYGAAPSTDGKVFCMPYALLGI 118
		Db 309 RKRHRHAKNRKGDRGSEWMTSSALPAATTMATICGNTVPTPIGLRACVLFAFGA 368
		Query 249 INNEKEYWKEDIEKEMLHYSEKLYKAFAKEQVTRYSVDTRTIGFEGSSYSEADETGDSE 308
		Db 68 RLKPHKAG-----VQWRFAGSFYPAITVTTIGYGAAPSTDGKVFCMPYALLGI 118
		Db 309 RKRHRHAKNRKGDRGSEWMTSSALPAATTMATICGNTVPTPIGLRACVLFAFGA 368
		Query 249 INNEKEYWKEDIEKEMLHYSEKLYKAFAKEQVTRYSVDTRTIGFEGSSYSEADETGDSE 308
		Db 68 RLKPHKAG-----VQWRFAGSFYPAITVTTIGYGAAPSTDGKVFCMPYALLGI 118
		Db 309 RKRHRHAKNRKGDRGSEWMTSSALPAATTMATICGNTVPTPIGLRACVLFAFGA 368
		Query 249 INNEKEYWKEDIEKEMLHYSEKLYKAFAKEQVTRYSVDTRTIGFEGSSYSEADETGDSE 308
		Db 68 RLKPHKAG-----VQWRFAGSFYPAITVTTIGYGAAPSTDGKVFCMPYALLGI 118
		Db 309 RKRHRHAKNRKGDRGSEWMTSSALPAATTMATICGNTVPTPIGLRACVLFAFGA 368
		Query 249 INNEKEYWKEDIEKEMLHYSEKLYKAFAKEQVTRYSVDTRTIGFEGSSYSEADETGDSE 308
		Db 68 RLKPHKAG-----VQWRFAGSFYPAITVTTIGYGAAPSTDGKVFCMPYALLGI 118
		Db 309 RKRHRHAKNRKGDRGSEWMTSSALPAATTMATICGNTVPTPIGLRACVLFAFGA 368
		Query 249 INNEKEYWKEDIEKEMLHYSEKLYKAFAKEQVTRYSVDTRTIGFEGSSYSEADETGDSE 308
		Db 68 RLKPHKAG-----VQWRFAGSFYPAITVTTIGYGAAPSTDGKVFCMPYALLGI 118
		Db 309 RKRHRHAKNRKGDRGSEWMTSSALPAATTMATICGNTVPTPIGLRACVLFAFGA 368
		Query 249 INNEKEYWKEDIEKEMLHYSEKLYKAFAKEQVTRYSVDTRTIGFEGSSYSEADETGDSE 308
		Db 68 RLKPHKAG-----VQWRFAGSFYPAITVTTIGYGAAPSTDGKVFCMPYALLGI 118
		Db 309 RKRHRHAKNRKGDRGSEWMTSSALPAATTMATICGNTVPTPIGLRACVLFAFGA 368
		Query 249 INNEKEYWKEDIEKEMLHYSEKLYKAFAKEQVTRYSVDTRTIGFEGSSYSEADETGDSE 308
		Db 68 RLKPHKAG-----VQWRFAGSFYPAITVTTIGYGAAPSTDGKVFCMPYALLGI 118
		Db 309 RKRHRHAKNRKGDRGSEWMTSSALPAATTMATICGNTVPTPIGLRACVLFAFGA 368
		Query 249 INNEKEYWKEDIEKEMLHYSEKLYKAFAKEQVTRYSVDTRTIGFEGSSYSEADETGDSE 308
		Db 68 RLKPHKAG-----VQWRFAGSFYPAITVTTIGYGAAPSTDGKVFCMPYALLGI 118
		Db 309 RKRHRHAKNRKGDRGSEWMTSSALPAATTMATICGNTVPTPIGLRACVLFAFGA 368
		Query 249 INNEKEYWKEDIEKEMLHYSEKLYKAFAKEQVTRYSVDTRTIGFEGSSYSEADETGDSE 308
		Db 68 RLKPHKAG-----VQWRFAGSFYPAITVTTIGYGAAPSTDGKVFCMPYALLGI 118
		Db 309 RKRHRHAKNRKGDRGSEWMTSSALPAATTMATICGNTVPTPIGLRACVLFAFGA 368
		Query 249 INNEKEYWKEDIEKEMLHYSEKLYKAFAKEQVTRYSVDTRTIGFEGSSYSEADETGDSE 308
		Db 68 RLKPHKAG-----VQWRFAGSFYPAITVTTIGYGAAPSTDGKVFCMP

R.Gattung, S.; Wu, X.  
Submitted to the EMBL Data Library, March 1996  
A; Description: The sequence of *C. elegans* cosmid F20A1.

A; Reference number: Z20726

A; Accession: T30037

A; Status: preliminary; translated from GB/EMBL/DBBJ

A; Molecule type: DNA

A; Residues: 1-1539 <GAT>

A; Cross-references: UNIPROT:Q19511; EMBL:U53150; PIDN:AAA96127.1; GSPDB:GN00023; CESP:F2

A; Experimental source: strain Bristol N2; clone F20A1

C; Genetics:

A; Gene: CESP:F20A1.7

A; Map position: 5

A; Intron: 19/3; 41/2; 71/2; 110/3; 135/2; 190/1; 246/1; 287/3; 491/3; 598/2; 983/2; 110

Score Match

13.1%;

Best Local Similarity 24.6%;

Pred. No. 1\_3e-15;

Matches 60;

Mismatches 126;

Indels 108;

Gaps 13;

A; Map position: 5

A; Intron: 13/3; 41/2; 71/2; 110/3; 135/2; 190/1; 246/1; 287/3; 491/3; 598/2; 983/2; 110

Score 2.68;

DB 2;

Length 1539;

Qy

8 TLALIVCTFTYLGVAAVFDALESEPELIERQ-----RLELRQQELRA-RYNLSQQG 58

Db

88 TPKLILITGLYSFGAHFTMYLEVPTDIBAREDFHQRKIAFREVMVNLRAFYDNEDR 147

Qy

59 YEBLERVVLRLKPHKAGIQ-----WRFAGPSFYFAITVITITGYGAHAPSTDGGKVFCM 111

Db

148 EERWKHALLKFE-EDIGLEEPVIEPTVNTFWMSFLYAGTIFTIYGNGNACKTRAGQLT 206

Qy

112 FYALGIGLTFYMLVQSL-----GERI-----

Db

207 VYAFVGIPIMLVNLTSNLNFNLKWLKLTINGSDMTLYIGVRLGITYTQDEVQKLRLYT 266

Qy

133 ---NTLVRYLL--HRAKNGLMGRADVSANM-----

Db

267 KLTAKTMKWKLPSKGAPSIALNSEERNLNSTPESDDBEETIHQDPVLSPLIATAWI 326

Qy

172 CIGAAAPHSHYEHTTEFAQYYCPITLITGFDYVALQKDQALQTQPOCYVAFSFVYLTG 231

Db

327 ILSAAVFCLFEDWTFFTSYFCFTSLTGTGD-----VTPANPEYMLATEFGVVIVG 378

Qy

232 LTVIGAFNLVVRFMNTNAEDEKRDAHRLTRNGAGGGGGSSAHTTDASSTAA 291

Db

379 LSNLTVVCIDVQBLQKLAQNM-----AIQLKLTEYMEAVKSG-----DPNASAMMA 425

Qy

292 GCGG-----FRNVYAEVL-HFQSNCs 311

Db

426 GFGRAKFLMLPLISKNEGAKMDKFQDCS 455

Qy

T21598

hypothetical protein F31D4.7 - Caenorhabditis elegans

C; Species: Caenorhabditis elegans

C; Accession: T21598

R; Mortimore, B.

Submitted to the EMBL Data Library, March 1997

A; Reference number: Z9447

A; Gene: CESP:F31D4.7

A; Map position: 5

A; Intron: 13/3; 90/2; 149/1; 222/3; 290/3

Db	17 LIVFLIYCISGGVFLVPLIBEPYQSELRAQHKIENNRARTVDAWMKKIFNNSDVLYI 76
Qy	57 -----EGYEELERVVLKPHKAGYVQWRFAGPSFYFAITVITITGYGHAA 100
Db	77 KGNTSQRLTTFFTELEGSYEN---QIGVKWSQQKNDWFNNAVLPAFTCTIGYGHY 132
Qy	101 PSTDGGKVFCMFYALUGIPLTLMFOSLGERINTVRYLLHRAKGL-----
Db	133 PTDAGRMLTMIFALFGPLMLVQDGFKLTTIRPWFQIKRLMRIMCCTKQPIE 192
Qy	148 -----GMRRADYVSAMMV-LIGFPCSCISTLCIGAAFSHYEH-WTFQOAYYYCFITLT 199
Db	193 EMKEIERHQHLDIFDPLPVGLALIVTWICSFVLSYMDHNWTLESPFVFTPLST 252
Qy	200 IGRGDYALQDQALQTOPQYAFSPYVLTGIGLIGAFLNLVVLRLT 256
Db	253 VGLGDLV-----PSSPRLLITMFQGFLVGSLSVSMVINELQAKMKSTYBAGRNDK 304
Qy	257 DAERHALLTRNG 268
Db	305 PHHQTLPTSLG 316

RESULT 13	Qy	13.1%; Score 2.68; DB 2; Length 1539; Best Local Similarity 24.6%; Pred. No. 1_3e-15; Matches 60; Mismatches 126; Indels 108; Gaps 13; A; Map position: 5; A; Intron: 13/3; 41/2; 71/2; 110/3; 135/2; 190/1; 246/1; 287/3; 491/3; 598/2; 983/2; 110
T13807	potassium channel protein - fruit fly (Drosophila melanogaster)	
Qy	Species: Drosophila melanogaster	
Db	Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004	
Qy	C; Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004	
Db	C; Accession: T13807	
Qy	C; Species: Price, L.A.; Rosenthal, D.N.; Pausch, M.H.	
Db	R; Goldstein, S.A.; Proc. Natl. Acad. Sci. U.S.A. 93, 13256-13261, 1996	
Qy	A; Title: ORK1, a potassium-selective leak channel with two pore domains cloned from <i>Drosophila</i>	
Db	A; Reference number: 217770; PMID: 9707515;	
Qy	A; Accession: T13807	
Db	A; Status: preliminary; translated from GB/EMBL/DBDJ	
Qy	A; Molecular type: mRNA	
Db	A; Residues: 1-1001 <COL>	
Qy	A; Cross-references: UNIPROT:Q94526; EMBL:U55321; PID:q3808067; PID:93808068; PID: AAC69.	
Db	A; Gene: ORK1	
Qy	A; Cross-references: FlyBase:FBgn0017561	
Db	A; Map position: 1	
Qy	Query Match 12.8%; Score 261.5; DB 2; Length 1001; Best Local Similarity 25.0%; Pred. No. 3e-15; Matches 65; Mismatches 107; Indels 35; Gaps 8;	
Db	7 RPLALIVCTFTYLGVAVDALSSEPELIERQRLERQQLRNLUSQGYEL----	
Qy	5 RWLILLPFYISVLFQGAIYHIEHGEKIS-----RAEQRKQIAINEYLLBDKN 58	
Db	5 RPLALIVCTFTYLGVAVDALSSEPELIERQRLERQQLRNLUSQGYEL----	
Qy	63 -----KPL-----KP-----HKAGVQWRFAGPSFYFAITVITITGYGHAA 106	
Db	59 TTQDEBTLQRISDYCDPVTLPDTPTWTFHAFPTVCSTVGNISPTFAG 118	
Qy	107 KVFCMFYALGIPLTLMFOSLGERINTVRYLLHRAK-----GLGMRRAVDVSMANVL 161	
Db	119 RMIMIAVSGIPVNGTILFAGLEYFGRTEIYRRKYYKMSDTHYVPPOLGLITVV 178	
Qy	162 IGFFCSC-ST-LGIGAAFSHYEHWTFFQAYYYCFITLTIGGDDYV-ALQDQALQTOPQ 219	
Db	179 IALPGIALFLPLPSWVFTYPENNPIISLYSYVTTTIGSDYVPTFGANQKBFGGW 238	
Qy	220 YVAFSFYVILTGTVGAFLNLVVLRFMTMNAEDEK 255	
Db	S44635 f22b7.7 protein - Caenorhabditis elegans	
Qy	239 FVYQIFVIVWFISLGYL-----WMMTFITRGLQSKK 272	

RESULT 14	Qy	12.8%; Score 262; DB 2; Length 443; Best Local Similarity 25.0%; Pred. No. 1e-15; Matches 55; Mismatches 113; Indels 66; Gaps 9; A; Map position: 5; A; Intron: 13/3; 90/2; 149/1; 222/3; 290/3
T21598	hypothetical protein F31D4.7 - Caenorhabditis elegans	
Qy	C; Species: Caenorhabditis elegans	
Db	C; Accession: T21598	
Qy	R; Mortimore, B.	
Db	Submitted to the EMBL Data Library, March 1997	
Qy	A; Reference number: Z9447	
Db	A; Gene: CESP:F31D4.7	
Qy	A; Map position: 5	
Db	A; Experimental source: Clone F31D4	
Qy	C; Genetics:	
Db	A; Cross-references: UNIPROT:O45422; EMBL:Z92832; PIDN:CAE07375.1; GSPDB:GN00023; CESP:F3	
Db	11 LIVCTFTYLGVAVFDDALES--EPEL-----IERORLRLRQQELRARYNLSQL---	



Result No.	Score	Query Match Length DB ID	Description
1	2042	100.0 394 9 US-09-930-484-4	Sequence 4, Appli
2	2042	100.0 394 9 US-09-930-483-4	Sequence 4, Appli
3	2042	100.0 394 9 US-09-798-584-15	Sequence 15, Appli
4	2042	100.0 394 14 US-10-146-733-17	Sequence 17, Appli
5	2042	100.0 394 14 US-10-146-733-18	Sequence 18, Appli
6	2042	100.0 395 14 US-10-146-733-8	Sequence 8, Appli
7	1850.5	90.6 412 14 US-10-146-733-9	Sequence 9, Appli
8	1819	89.1 405 9 US-09-930-484-5	Sequence 5, Appli
9	1819	89.1 405 9 US-09-930-483-5	Sequence 5, Appli
10	1278	62.6 258 9 US-09-744-491-61	Sequence 61, Appli
11	1224	59.9 312 17 US-10-870-492-55	Sequence 55, Appli
12	1224	59.9 233 15 US-10-459-190-15	Sequence 15, Appli
13	1154	56.5 374 14 US-09-798-584-1	Sequence 1, Appli
14	1116	54.7 374 14 US-10-146-733-41	Sequence 41, Appli
15	1116	54.7 374 15 US-10-257-022-6	Sequence 6, Appli
16	1116	54.7 374 15 US-10-074-978A-194	Sequence 194, Appli
17	1116	54.7 374 15 US-10-074-978A-195	Sequence 195, Appli
18	1077.5	52.8 387 9 US-09-746-491-60	Sequence 60, Appli
19	1069.5	52.4 365 9 US-09-746-491-60	Sequence 59, Appli
20	846	41.4 320 9 US-09-746-491-59	Sequence 59, Appli
21	846	41.4 330 15 US-10-336-472-76	Sequence 42, Appli
22	846	41.4 330 15 US-10-074-978A-192	Sequence 192, Appli
23	846	41.4 330 15 US-10-074-978A-193	Sequence 193, Appli
24	846	41.4 400 14 US-10-146-733-5	Sequence 5, Appli
25	838	41.0 330 9 US-09-746-491-58	Sequence 58, Appli
26	838	41.0 330 15 US-10-074-978A-191	Sequence 191, Appli
27	838	41.0 330 15 US-10-336-472-76	Sequence 76, Appli
28	838	41.0 393 9 US-09-746-491-22	Sequence 22, Appli
29	838	41.0 400 14 US-10-146-733-2	Sequence 2, Appli
30	838	41.0 400 15 US-10-257-022-13	Sequence 13, Appli
31	774	37.9 279 9 US-09-864-761-34389	Sequence 34389, A
32	619	30.3 212 15 US-10-074-978A-24	Sequence 24, Appli
33	507.5	24.9 179 15 US-10-124-593-21617	Sequence 216417,
34	370	18.1 370 9 US-09-930-484-8	Sequence 8, Appli
35	370	18.1 370 9 US-09-930-483-8	Sequence 8, Appli
36	365.9	18.1 411 9 US-09-828-746-6	Sequence 6, Appli
37	365.5	17.9 295 16 US-10-143-903-8	Sequence 8, Appli
38	366	17.9 487 17 US-10-161-862-129	Sequence 129, Appli
39	364	17.8 422 16 US-10-319-528-20	Sequence 20, Appli
40	364	17.8 426 8 US-08-816-011-45	Sequence 45, Appli
41	364	17.8 426 17 US-10-870-492-45	Sequence 2, Appli
42	363	17.8 411 9 US-09-828-746-2	Sequence 18, Appli
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## ALIGNMENTS

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 Gapop 10.0 , Gapext 0.5  
 Perfect score: 2042  
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 Run on: July 13, 2005, 08:40:02 ; Search time 86.5115 Seconds  
 (without alignment)  
 1759.475 Million cell updates/sec

Title: US-09-503-089A-5  
 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : Published Applications AA:  
 1: /cgns\_6/\_ptodata/1/pubcaa/US07\_PUBCOMB.pep.\*  
 2: /cgns\_6/\_ptodata/1/pubcaa/PCN\_NEW\_PUB.pep.\*  
 3: /cgns\_6/\_ptodata/1/pubcaa/US06\_NEW\_PUB.pep.\*  
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 22: /cgns\_6/\_ptodata/1/pubcaa/US60\_FUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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2	2042	100.0 394 9 US-09-930-483-4	Sequence 4, Appli
3	2042	100.0 394 9 US-09-798-584-15	Sequence 15, Appli
4	2042	100.0 394 14 US-10-146-733-17	Sequence 17, Appli
5	2042	100.0 394 14 US-10-146-733-18	Sequence 18, Appli
6	2042	100.0 395 14 US-10-146-733-8	Sequence 8, Appli
7	1850.5	90.6 412 14 US-10-146-733-9	Sequence 9, Appli
8	1819	89.1 405 9 US-09-930-484-5	Sequence 5, Appli
9	1819	89.1 405 9 US-09-930-483-5	Sequence 5, Appli
10	1278	62.6 258 9 US-09-744-491-61	Sequence 61, Appli
11	1224	59.9 312 8 US-08-816-011-55	Sequence 55, Appli

Result No.	Score	Query Match Length DB ID	Description
1	2042	100.0 394 9 US-09-930-484-4	Sequence 4, Appli
2	2042	100.0 394 9 US-09-930-483-4	Sequence 4, Appli
3	2042	100.0 394 9 US-09-798-584-15	Sequence 15, Appli
4	2042	100.0 394 14 US-10-146-733-17	Sequence 17, Appli
5	2042	100.0 394 14 US-10-146-733-18	Sequence 18, Appli
6	2042	100.0 395 14 US-10-146-733-8	Sequence 8, Appli
7	1850.5	90.6 412 14 US-10-146-733-9	Sequence 9, Appli
8	1819	89.1 405 9 US-09-930-484-5	Sequence 5, Appli
9	1819	89.1 405 9 US-09-930-483-5	Sequence 5, Appli
10	1278	62.6 258 9 US-09-744-491-61	Sequence 61, Appli
11	1224	59.9 312 8 US-08-816-011-55	Sequence 55, Appli

RESULT 1  
 US-09-339-484-4  
 ; Sequence 4, Application US/09939484  
 ; Patent No. US2002003232A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Duprat, Fabrice  
 ; ATTORNEY: Lesege, Florian  
 ; APPLICANT: Fink, Michel  
 ; APPLICANT: Lazdunski, Michel  
 ; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING  
 ; TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS  
 ; FILE REFERENCE: 1201-CIP-DIV-00  
 ; CURRENT FILING DATE: 2001-08-24  
 ; PRIOR APPLICATION NUMBER: US/09/939,484  
 ; PRIOR FILING DATE: 1998-09-01  
 ; PRIOR APPLICATION NUMBER: FR 96/01565  
 ; PRIOR FILING DATE: 1996-11-15  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 4  
 ; LENGTH: 394  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; OTHER INFORMATION: TASK  
 ; US-09-939-484-4  
 ; PRIORITY: Application Number: 60/095,234  
 ; PRIORITY FILING DATE: 1998-08-04  
 ; PRIORITY APPLICATION NUMBER: FR 96/01565  
 ; NUMBER OF SEQ ID NOS: 24  
 ; PRIORITY FILING DATE: 1996-02-08



Db 301 AEYLHFQGMCSCLWYKSRKLOYSIPMIIPRDLSTSPTCVEQSNSPGGGRYSDTPSRR 360  
 Qy 361 CLCGAPSAAISSVSTGHSLSFRGLMKRSSLV 394  
 Db 361 CLCGAPSAAISSVSTGHSLSFRGLMKRSSLV 394

**RESULT 4**  
 US-10-146-733-17  
 Sequence 17, Application US/10146733  
 Publication No. US20030165891A1  
 GENERAL INFORMATION:  
 APPLICANT: Curtis, Rory A.J.  
 APPLICANT: Glucksman, Maria A.  
 APPLICANT: Silos-Sant'ago, Inmaculada  
 TITLE OF INVENTION: NOVEL TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611, IC47615,  
 TITLE OF INVENTION: HNMDA-1, TWIK-9, alpha2delta-4, 54414, AND 53763 MOLECULES  
 TITLE OF INVENTION: AND USES THEREFOR  
 FILE REFERENCE: MN1-248  
 CURRENT APPLICATION NUMBER: US/10/146,733  
 CURRENT FILING DATE: 2002-05-15  
 PRIOR APPLICATION NUMBER: US 60/185,938  
 PRIOR FILING DATE: 2000-02-29  
 PRIOR APPLICATION NUMBER: US 09/515,520  
 PRIOR FILING DATE: 2000-02-29  
 PRIOR APPLICATION NUMBER: US 09/518,866  
 PRIOR FILING DATE: 2000-03-03  
 PRIOR APPLICATION NUMBER: US 60/195,734  
 PRIOR FILING DATE: 2000-04-07  
 PRIOR APPLICATION NUMBER: US 60/195,993  
 PRIOR FILING DATE: 2000-04-11  
 PRIOR APPLICATION NUMBER: US 60/199,799  
 PRIOR FILING DATE: 2000-04-26  
 PRIOR APPLICATION NUMBER: US 60/233,537  
 PRIOR FILING DATE: 2000-09-19  
 PRIOR APPLICATION NUMBER: US 60/235,018  
 PRIOR FILING DATE: 2000-09-25  
 PRIOR APPLICATION NUMBER: US 60/235,059  
 PRIOR FILING DATE: 2000-09-25  
 PRIOR APPLICATION NUMBER: US 60/256,240  
 PRIOR FILING DATE: 2000-12-15  
 PRIOR APPLICATION NUMBER: US 60/256,588  
 PRIOR FILING DATE: 2000-12-18  
 PRIOR APPLICATION NUMBER: US 60/258,028  
 PRIOR FILING DATE: 2000-12-21  
 PRIOR APPLICATION NUMBER: US 09/796,720  
 PRIOR FILING DATE: 2001-02-18  
 PRIOR APPLICATION NUMBER: US 09/828,035  
 PRIOR FILING DATE: 2001-04-06  
 PRIOR APPLICATION NUMBER: US 09/833,081  
 PRIOR FILING DATE: 2001-04-11  
 PRIOR APPLICATION NUMBER: US 09/843,128  
 PRIOR FILING DATE: 2001-04-25  
 PRIOR APPLICATION NUMBER: US 09/957,683  
 PRIOR FILING DATE: 2001-09-19  
 PRIOR APPLICATION NUMBER: US 09/964,252  
 PRIOR FILING DATE: 2001-09-25  
 PRIOR APPLICATION NUMBER: US 09/964,256  
 PRIOR FILING DATE: 2001-09-25  
 PRIOR APPLICATION NUMBER: US 10/024,623  
 NUMBER OF SEQ ID NOS: 85  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 17  
 LENGTH: 394  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 us-10-146-733-17

Query Match 100.0%; Score 2042; DB 14; Length 394;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-180;  
 Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MICROVORTLALIVCTFTYLLVGAAVDALESEPELIERQRLELRQELRQQELRQLRYNLSQGGYE 60  
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 Qy 61 ELERVVRLKPKHAKGIVQWRAGSFYFAITVITVIGYCHAAPSTDGGKVFCMPYFALLGTLPL 120  
 Db 61 ELERVVRLKPKHAKGIVQWRAGSFYFAITVITVIGYCHAAPSTDGGKVFCMPYFALLGTLPL 120  
 Qy 121 TLVMFQSILGERNTLVLLRAKKGJMGRADVSMMVNLIGPSCS1TLCGAAFSH 180  
 Db 121 TLVMFQSILGERNTLVLLRAKKGJMGRADVSMMVNLIGPSCS1TLCGAAFSH 180  
 Qy 181 YEHWTFFQAYYCFCITLTIGFGDYVALQDQALOTQOYVAFSFYVLTGTTVIGAFLN 240  
 Db 181 YEHWTFFQAYYCFCITLTIGFGDYVALQDQALOTQOYVAFSFYVLTGTTVIGAFLN 240  
 Qy 241 LVVLREMTMNADEKRDAEHLRALLTRNGQAGGGGGSAHTTDASSTAAGGGFPRNVY 300  
 Db 241 LVVLREMTMNADEKRDAEHLRALLTRNGQAGGGGGSAHTTDASSTAAGGGFPRNVY 300  
 Qy 301 AEVLHPQSMCSCLWYKSREKLOYSIPMIPIRDLSTSPTCVOBSSHSPRGGRYSDTPSRR 360  
 Db 301 AEVLHPQSMCSCLWYKSREKLOYSIPMIPIRDLSTSPTCVOBSSHSPRGGRYSDTPSRR 360  
 Qy 361 CLCGARSATSSVSGHSLSTFRGLMKRSSV 394  
 Db 361 CLCGARSATSSVSGHSLSTFRGLMKRSSV 394

**RESULT 5**  
 US-10-146-733-18  
 Sequence 18, Application US/10146733  
 Publication No. US20030165891A1  
 GENERAL INFORMATION:  
 APPLICANT: Curtis, Rory A.J.  
 APPLICANT: Gluckmann, Maria A.  
 APPLICANT: Silos-Santiago, Inmaculada  
 TITLE OF INVENTION: NOVEL TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611, IC47615,  
 TITLE OF INVENTION: HNMDA-1, TWIK-9, alpha2delta-4, 54414, AND 53763 MOLECULES  
 TITLE OF INVENTION: AND USES THEREFOR  
 FILE REFERENCE: MN1-248  
 CURRENT APPLICATION NUMBER: US/10/146,733  
 PRIOR APPLICATION NUMBER: US 60/185,938  
 PRIOR FILING DATE: 2000-02-29  
 PRIOR APPLICATION NUMBER: US 09/515,520  
 PRIOR FILING DATE: 2000-02-29  
 PRIOR APPLICATION NUMBER: US 09/518,866  
 PRIOR FILING DATE: 2000-03-03  
 PRIOR APPLICATION NUMBER: US 09/828,035  
 PRIOR FILING DATE: 2001-04-06  
 PRIOR APPLICATION NUMBER: US 09/833,081  
 PRIOR FILING DATE: 2001-04-11  
 PRIOR APPLICATION NUMBER: US 09/843,128  
 PRIOR FILING DATE: 2001-04-25  
 PRIOR APPLICATION NUMBER: US 09/957,683  
 PRIOR FILING DATE: 2001-09-19  
 PRIOR APPLICATION NUMBER: US 09/964,252  
 PRIOR FILING DATE: 2001-09-25  
 PRIOR APPLICATION NUMBER: US 09/964,256  
 PRIOR FILING DATE: 2001-09-25  
 PRIOR APPLICATION NUMBER: US 10/024,623  
 NUMBER OF SEQ ID NOS: 85  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 17  
 LENGTH: 394  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 us-10-146-733-17

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; PRIOR APPLICATION NUMBER: US 09/843,128
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 09/957,683
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: US 09/964,252
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 09/964,256
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 10/024,623
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 18
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-146-733-18

Query Match          100 %;  Score 2042;  DB 14;  Length 394;
Best Local Similarity 100 %;  Pred. No. 1. 4-e-180;
Matches 394;  Conservative 0;  Misnatches 0;  Gaps 0;

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Qy      61 ELERVYLRKPHKAGQWRFGSFYPAITVTTIGCHAAPSTDGKVFCMYFALLGIPL 120
Db      61 ELERVYLRKPHKAGQWRFGSFYPAITVTTIGCHAAPSTDGKVFCMYFALLGIPL 120

Qy      121 TLVMFSLGERINTLYRLLRKKGGLGMRRADVSANMVLIQFFSCISTLCLGAAAFSH 180
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Qy      181 YEHWTWFOAQYYCFITLTIGFGDYVALQDQALCOTOPQYVAFSFVYIILTGTVIGAFLN 240
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Qy      241 LVVLRFMTMNAEDEKDAEHRALLTNGQAGGGGGSAHTTDTASSTAAGGGFRNVY 300
Db      241 LVVLRFMTMNAEDEKDAEHRALLTNGQAGGGGGSAHTTDTASSTAAGGGFRNVY 300

Qy      301 ABVLHFQSMCSCLWYKSGREKLQYSIMPMIIPDLSTSDTCVEOSHSPGGGRYSDTPSRR 360
Db      301 ABVLHFQSMCSCLWYKSGREKLQYSIMPMIIPDLSTSDTCVEOSHSPGGGRYSDTPSRR 360

Qy      361 CLCGGAPRSAISSSVSTGLHSLSFRGLMKRSSV 394
Db      361 CLCGGAPRSAISSSVSTGLHSLSFRGLMKRSSV 394

RESULT 6
US-10-146-733-8
Sequence 8 ; Application US/10146733
Publication No. US20030165891A1
GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Gluchsmann, Maria A.
; APPLICANT: Silos-Santiago, Inmaculada
TITLE OF INVENTION: HNMDA-1, TWIK-7, IC23927, TWIK-8, IC47611, IC47615, alpha2Delta-4, 54414, AND 53763 MOLECUL
TITLE OF INVENTION: HNMDA-1, TWIK-9, alpha2Delta-4, 54414, AND 53763 MOLECUL
TITLE OF INVENTION: FILE REFERENCE: MNI-248
CURRENT APPLICATION NUMBER: US/10/146,733
CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US 60/185,938
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: US 09/515,520
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: US 09/518,866
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: US 60/195,734
; PRIOR FILING DATE: 2000-04-07

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RESULT 7  
 US-10-146-733-9  
 Sequence 9, Application US/10146733  
 Publication No. US20030165891A1  
 GENERAL INFORMATION:  
 APPLICANT: Curtis, Rory A.J.  
 APPLICANT: Glucksmann, Maria A.  
 APPLICANT: Silos-Santago, Inmaculada  
 TITLE OF INVENTION: NOVEL TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611, IC47615,  
 TITLE OF INVENTION: HNMDA-1, TWIK-9, alpha2delta-4, 54414, AND 53763 MOLECULES  
 FILE REFERENCE: MN1-248  
 CURRENT FILING DATE: US/10/146-733  
 PRIOR APPLICATION NUMBER: US 60/165, 938  
 PRIOR FILING DATE: 2002-05-15  
 PRIOR APPLICATION NUMBER: US 60/165, 938  
 PRIOR FILING DATE: 2000-02-29  
 PRIOR APPLICATION NUMBER: US 09/515, 520  
 PRIOR FILING DATE: 2000-02-29  
 PRIOR APPLICATION NUMBER: US 09/518, 866  
 PRIOR FILING DATE: 2000-03-03  
 PRIOR APPLICATION NUMBER: US 60/195, 734  
 PRIOR FILING DATE: 2000-04-07  
 PRIOR APPLICATION NUMBER: US 60/195, 993  
 PRIOR FILING DATE: 2000-04-11  
 PRIOR APPLICATION NUMBER: US 60/199, 799  
 PRIOR FILING DATE: 2000-04-26  
 PRIOR APPLICATION NUMBER: US 60/233, 537  
 PRIOR FILING DATE: 2000-09-19  
 PRIOR APPLICATION NUMBER: US 60/235, 018  
 PRIOR FILING DATE: 2000-09-25  
 PRIOR FILING DATE: 2000-09-25  
 PRIOR FILING DATE: 2000-12-15  
 PRIOR APPLICATION NUMBER: US 60/256, 588  
 PRIOR FILING DATE: 2000-12-18  
 PRIOR FILING DATE: 2000-12-21  
 PRIOR APPLICATION NUMBER: US 09/796, 720  
 PRIOR FILING DATE: 2001-02-28  
 PRIOR APPLICATION NUMBER: US 09/828, 035  
 PRIOR FILING DATE: 2001-04-06  
 PRIOR APPLICATION NUMBER: US 09/833, 081  
 PRIOR FILING DATE: 2001-04-11  
 PRIOR APPLICATION NUMBER: US 09/843, 128  
 PRIOR FILING DATE: 2001-04-25  
 PRIOR APPLICATION NUMBER: US 09/957, 683  
 PRIOR FILING DATE: 2001-09-19  
 PRIOR FILING DATE: 2001-09-25  
 PRIOR APPLICATION NUMBER: US 09/964, 252  
 PRIOR FILING DATE: 2001-09-25  
 PRIOR APPLICATION NUMBER: US 10/024, 623  
 NUMBER OF SEQ ID NOS: 85  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 9

Query Match 90.6%; Score 1850.5; DB 14; Length 412;  
 Best Local Similarity 88.3%; Pred. No. 8.3e-23; Indels 17; Gaps 2;  
 TYPE: PRT  
 ORGANISM: Rattus norvegicus  
 US-10-146-733-9

Query Match 90.6%; Score 1850.5; DB 14; Length 412;  
 Best Local Similarity 88.3%; Conservatve 8; Mismatches 23; Indels 17; Gaps 2;  
 TYPE: PRT  
 ORGANISM: Elervvrlkphkagvqragsfyyfafitittigxhaapstdggkvcmfyallgipl 120  
 DB 62 Elervvrlkphkagvqragsfyyfafitittigxhaapstdggkvcmfyallgipl 121

Qy 1 MRQNVRTRIALIVCTFTLVLGRAVFDALESEPELIERQRLELRQERARYNLNSQGYE 60  
 DB 2 MRQNVRTRIALIVCTFTLVLGRAVFDALESEPEMIEQRLELRQERARYNLNSQGYE 61

Qy 121 TLVMFOSLGERINTLVRYLHLRAKKGLGMRRADYSSMAMMVLTGFSCSITCIGAAAFSH 180  
 Db 122 TLVMFOSLGERINTFVYLLHLRAKKGLGMRAEVSMANMVLCIGFSCLSTLCIGAAFSY 181  
 Qy 181 YEWTFPQAYYCIPITLTIGGDTVALQDQALOTQPOQYVAFSFVYILTGLTVIGAPLN 240  
 Db 182 YEWTFPQAYYCIPITLTIGFDDVALQDQALOTQPOQYVAFSFVYILTGLTVIGAPLN 241  
 Qy 241 LVVLRFMTMNAEDEKRDAEHLRAILTRNGQAGGGG-----GSAAHTTDATASSTA 291.  
 Db 242 LVVLRFMTMNAEDEKRDAEHLRAILTRNGQAGGGG-----GSAAHTTDATASSTA 301.  
 Qy 292 -----GGGFRNYYAEVTLHQSMCSCLMVKSRKLQYSIPMIIIPRDLSTSSTDTCYBQS 343  
 Db 302 GMGVGVGGSGFRNYYAEMLHQSMCSCLMVKSRKLQYSIPMIIIPRDLSTSSTDTCYBHS 361  
 Qy 344 HSSPGGGRYSDTPSPRCLCGAPSRAISSVSTGLHSLSFTGLMRKRSV 394  
 Db 362 HSSPGGGRYSDTPSPHPLCSTGORSASSVSTGLHSLSFTGLMRKRSV 412

RESULT 8  
 US-09-939-484-5  
 Sequence 5, Application US/09939484  
 ; Patent No. US20032322A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Duprat, Fabrice  
 ; APPLICANT: Lesage, Florian  
 ; APPLICANT: Pink, Michel  
 ; APPLICANT: Lazdunski, Michel  
 ; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING  
 ; TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS  
 ; FILE REFERENCE: 1201-CLP-DIV-00  
 ; CURRENT APPLICATION NUMBER: US/09/939,484  
 ; CURRENT FILING DATE: 2001-08-24  
 ; PRIOR APPLICATION NUMBER: 09/144,914  
 ; PRIOR FILING DATE: 1998-09-01  
 ; PRIOR APPLICATION NUMBER: 08/749,816  
 ; PRIOR FILING DATE: 1996-11-15  
 ; PRIOR APPLICATION NUMBER: 60/095,234  
 ; PRIOR FILING DATE: 1998-08-04  
 ; PRIOR APPLICATION NUMBER: PR 96/01565  
 ; PRIOR FILING DATE: 1996-02-08  
 ; NUMBER OF SEQ ID NOS: 24  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 5  
 ; LENGTH: 405  
 ; TYPE: PRT  
 ; ORGANISM: Murine  
 ; FEATURE:  
 ; OTHER INFORMATION: TASK  
 US-09-939-484-5

Query Match 89.1%; Score 1819; DB 9; Length 405;  
 Best Local Similarity 88.1%; Pred. No. 6.8e-160;  
 Matches 357; Conservative 9; Mismatches 25; Indels 14; Gaps 2;

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 Qy 64 RVVRLKPHKAGVQRAGSFYYFAITTTGHAAPSTDGGKVCMFYALLGIPLTLI 123  
 Db 61 RVVRLKPHKAGVQRAGSFYYFAITTTGHAAPSTDGGKVCMFYALLGIPLTLI 120  
 Qy 124 MFQSLGERINTLVYLLHLRAKKGLGMRAEVSMANMVLCIGFSCLSTLCIGAAFSYEH 183  
 Db 121 MFQSLGERINTLVYLLHLRAKKGLGMRAEVSMANMVLCIGFSCLSTLCIGAAFSYER 180

Qy 184 WTEFOAYYCIPITLTIGGDTVALQDQALOTQPOQYVAFSFVYILTGLTVIGAFLNLVV 243  
 Db 181 WTEFOAYYCIPITLTIGGDTVALQDQALOTQPOQYVAFSFVYILTGLTVIGAFLNLVV 240

244 LRFMTINADEKDAEHRALTRNGAGGGG-----GGSAAHTIDTASSTAA----- 291  
 Qy : ||||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
 Db : 244 LRFMTINADEKDAEHRALTRNGAGGGG-----GGSAAHTIDTASSTAA----- 291  
 Qy : ||||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
 Db : 245 -GGGPFPRNTAEVLFQSMCCLWTKSREKLYQSTPMIIPRDLSTSDETCYEQSHSSPGG 349  
 Qy : ||||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
 Db : 301 GVGGSFRNTAEVLFQSMCCLWTKSREKLYQSTPMIIPRDLSTSDETCYEHSHSSPGG 360  
 Qy : ||||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
 Db : 361 GGRYSDTPSHPCLCGTQRSATSSVTLHSLAAFRGLMKRSSV 405  
 RESULT 9  
 US-09-939-483-5  
 Sequence 5; Application US/09939483  
 Pctn No. US2009455A1  
 GENERAL INFORMATION:  
 APPLICANT: Duprat, Fabrice  
 APPLICANT: Lesage, Florian  
 APPLICANT: Pink, Michel  
 APPLICANT: Lazdunski, Michel  
 TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS  
 FILE REFERENCE: 12011-CIP-DIV-2-00  
 CURRENT APPLICATION NUMBER: US/09/939,483  
 CURRENT FILING DATE: 2001-08-24  
 PRIOR APPLICATION NUMBER: 09/144,914  
 PRIOR FILING DATE: 1998-09-01  
 PRIOR APPLICATION NUMBER: 08/749,816  
 PRIOR FILING DATE: 1996-11-15  
 PRIOR APPLICATION NUMBER: 60/095,234  
 PRIOR FILING DATE: 1998-08-14  
 PRIOR APPLICATION NUMBER: FR 96/01565  
 PRIOR FILING DATE: 1996-02-08  
 NUMBER OF SEQ ID NOS: 24  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 5  
 LENGTH: 405  
 TYPE: PRT  
 ORGANISM: Murine  
 FEATURE: Murine  
 OTHER INFORMATION: TASK  
 us-09-939-483-5

Query Match Score 89.1%; DB 9; Length 405;  
 Best Local Similarity 88.1%; Pred. No. 6 8e-160;  
 Matches 357; Conservative 9; Mismatches 25; Indels 14; Gaps 2;

Db : 4 ONVRTALIVCFTYLIVGAAVEDATESEPELJERORLELROELPARYNLSOGGYYEEL 63  
 Qy : !:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
 Db : 1 ENVRTALIVCFTYLIVGAAVEDATESEPELJERORLELROELPARYNLSOGGYYEEL 60  
 Qy : 64 RYVRLRKPHKAGYQWRPGSFPAITYTTGHAAPSTDGKVFCMFLGTLTV 123  
 Db : 61 RYVRLRKPHKAGYQWRPGSFPAITYTTGHAAPSTDGKVFCMFLGTLTV 120  
 Qy : 124 MFQSLGERINTFLYLLHRAKGLMERADYSMANVLYIGFSCISTLICGAAGFHYEH 183  
 Db : 121 MFQSLGERINTFLYLLHRAKGLMERADYSMANVLYIGFSCISTLICGAAGFYYER 180  
 Qy : 184 WTEFOQAYTCFITLTTIGFDYVALQDQALOTOPQYAFSPVYILTGTVGAFLNV 243  
 Db : 181 WTEFOQAYTCFITLTTIGFDYVALQDQALOTOPQYAFSPVYILTGTVGAFLNV 240  
 Qy : 244 LRFMTINADEKDAEHRALTRNGAGGGG-----GGSAAHTIDTASSTAA---- 291  
 Db : 241 LRFMTINADEKDAEHRALTRNGAGGGG-----GGSAAHTIDTASSTAA---- 291  
 Qy : ||||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
 Db : 301 GVGGSFRNTAEVLFQSMCCLWTKSREKLYQSTPMIIPRDLSTSDETCYEHSHSSPGG 360

Qy : 350 GGRYSDTPSHPCLCGTQRSATSSVTLHSLAAFRGLMKRSSV 394  
 Db : 361 GGRYSDTPSHPCLCGTQRSATSSVTLHSLAAFRGLMKRSSV 405

RESULT 10  
 US-09-746-491-61  
 Sequence 61; Application US/09746491  
 Patent No. US200137202A1  
 GENERAL INFORMATION:  
 APPLICANT: Burgess, Catherine E.  
 TITLE OF INVENTION: No. US200137202A1 Proteins and Nucleic Acids Encoding Same  
 FILE REFERENCE: 15966-621  
 CURRENT APPLICATION NUMBER: US/09/746,491  
 CURRENT FILING DATE: 2000-12-20  
 PRIOR APPLICATION NUMBER: USSN 60/171,329  
 PRIOR FILING DATE: 1999-12-21  
 NUMBER OF SEQ ID NOS: 72  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 61  
 LENGTH: 258  
 TYPE: PRT  
 ORGANISM: Mus musculus  
 us-09-746-491-61

Query Match Score 62.6%; DB 9;  
 Best Local Similarity 96.1%; Pred. No. 5.7e-110;  
 Matches 248; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Db : 1 MKRQNYRTLALIVCFTYLIVGAAVEDATESEPELJERORLELROELPARYNLSOGGYY 60  
 Qy : 1 MKRQNYRTLALIVCFTYLIVGAAVEDATESEPELJERORLELROELPARYNLSOGGYY 60  
 Db : 1 MKRQNYRTLALIVCFTYLIVGAAVEDATESEPELJERORLELROELPARYNLSOGGYY 60  
 Qy : 61 ELERVYVRLRKPHKAGYQWRPGSFPAITYTTGHAAPSTDGKVFCMFLGTLTV 120  
 Db : 61 ELERVYVRLRKPHKAGYQWRPGSFPAITYTTGHAAPSTDGKVFCMFLGTLTV 120  
 Qy : 121 TLVMFOSLGERINTFLYLLHRAKGLGMRRADYSMANVLYIGFSCISTLICGAAGAFSH 180  
 Db : 121 TLVMFOSLGERINTFLYLLHRAKGLGMRRADYSMANVLYIGFSCISTLICGAAGAFSH 180  
 Qy : 181 YEHWTTSFOQAYTCFITLTTIGFDYVALQDQALOTOPQYAFSPVYILTGTVGAFLN 240  
 Db : 181 YERWTTSFOQAYTCFITLTTIGFDYVALQDQALOTOPQYAFSPVYILTGTVGAFLN 240

RESULT 11  
 US-08-816-011-55  
 Sequence 55; Application US/08816011  
 Publication No. US20030165806A1  
 GENERAL INFORMATION:  
 APPLICANT: Pausch, Mark H.  
 TITLE OF INVENTION: Potassium Channels, Nucleotide Sequences and Methods of Using Same  
 NUMBER OF SEQUENCES: 56  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: American Home Products Corporation  
 STREET: One Campus Drive  
 CITY: Parsippany  
 STATE: New Jersey  
 COUNTRY: USA  
 ZIP: 07054  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/Ms-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/816,011  
 FILING DATE: 11 MAR 1997  
 CLASSIFICATION: 536  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Matthews, Gale P.  
 REFERENCE/DOCKET NUMBER: 32,421-C2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201-683-2134  
 TELEFAX: 201-603-4117  
 INFORMATION FOR SEQ ID NO: 55:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 312 amino acids  
 TYPE: amino acid  
 STRANDBNESS: single  
 TOPOLOGY: linear  
 US-08-816-011-55

Query Match 59.9%; Score 1224; DB 8; Length 312;  
 Best Local Similarity 83.1%; Pred. No. 7.4e-105; Indels 16; Gaps 4;  
 Matches 250; Conservative

Qy 4 QNVRTLAIJCTFTYLGAAVDALESEPELIERQELRQQLRAYNLNSOGGYYEEL 63  
 Db 13 ENVTLLAVCITYLLGAAVDALESEPEMIEQRQELRQQLRAYNLNSOGGYYEEL 72

Qy 64 RYVRLRKPAGQWRFGSFYPAITVTTIGYHAAPSTDGGKV--FCMFYALLGPL 120  
 Db 73 RYVRLRKPAGQWRFGSFYPAITVTTIGYHAAPSTDGGKVFCMFYALLGPL 132

Qy 121 TLWFOSLGERINTLVRLHAKKGMRADYSMANVLTGFSCSTLCTGAAAFSH 180  
 Db 133 TLWFOSLGERINTSVRLHAKKGMRADYSMANVLTGFSCSTLCTGAAAFSY 192

Qy 181 YEWTFQAYYCPTIITGFDYVAQDQLQTQOQYVAFSFTVLTGLTIVG-AF 238  
 Db 193 YEWTFQAYYCPTIITGFDYVAQDQLQTQOQYVAFSFTVLTGLTIVG-AF 239

Qy 239 LNVLVRFMNTMAEDERDAEHRAILTRNGAOGGGG-----GSAHTTDTASSTAA 290  
 Db 250 LNVLVRFMNTMAEDERDAEHRAILTRNGAOGGGG-----GSAHTTDTASSTAA 309

Qy 291 A 291  
 Db 310 A 310

RESULT 13  
 US-10-459-190-15  
 Sequence 15, Application US/10459190  
 Publication No. US20040072216A1  
 GENERAL INFORMATION:  
 APPLICANT: Johnson, Jeffrey D.  
 APPLICANT: Palma, John F.  
 APPLICANT: Schweitzer, Anthony C.  
 APPLICANT: Metabolix, Inc.  
 APPLICANT: Blume, John E.  
 TITLE OF INVENTION: Methods and Compositions for Treating and Diagnosing  
 TITLE OF INVENTION: Diabetes  
 FILE REFERENCE: 016325-008210US  
 CURRENT APPLICATION NUMBER: US/10/459,190  
 CURRENT FILING DATE: 2003-06-10  
 PRIOR APPLICATION NUMBER: US 60/387,642  
 PRIOR FILING DATE: 2002-06-10  
 NUMBER OF SEQ ID NOS: 24  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 15  
 LENGTH: 233  
 TYPE: PRT  
 ORGANISM: Mus sp.  
 FEATURE:  
 OTHER INFORMATION: transmembrane (TM) and pore domains of mouse  
 TWK-related acid sensitive potassium channel 1  
 OTHER INFORMATION: (TASK-1)  
 US-10-459-190-15

Query Match 56.5%; Score 1154; DB 15; Length 233;  
 Best Local Similarity 95.7%; Pred. No. 1.6e-38; Indels 5; Gaps 0;  
 Matches 223; Conservative

Qy 7 RTLAIIVCTFTYLGAAVDALESEPELIERQELRQQLRAYNLNSOGGYYEELRVV 66  
 Db 1 RTLAIIVCTFTYLGAAVDALESEPEMIEQRQELRQQLRAYNLNSOGGYYEELRVV 60

Qy 67 LRKPKAGQWRFGSFYPAITVTTIGYHAAPSTDGGKVFCMFYALLGPLVMFO 126  
 Db 61 LRKPKAGQWRFGSFYPAITVTTIGYHAAPSTDGGKVFCMFYALLGPLVMFO 120

Qy 127 SLGERINTLVRLHAKKGMRADYSMANVLTGFSCSTLCTGAAAFSHYEHTWF 186

RESULT 12  
 US-10-870-492-55  
 Sequence 55, Application US/10870492  
 Publication No. US20050012165A1  
 GENERAL INFORMATION:  
 APPLICANT: PAUSCH, MARK H.  
 TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,  
 AND METHODS OF USING SAME  
 FILE REFERENCE: 01142.0114  
 CURRENT FILING DATE: 2004-06-18  
 PRIOR APPLICATION NUMBER: US/10/870,192  
 PRIOR APPLICATION NUMBER: US/09/503,849  
 PRIOR FILING DATE: 2000-02-15  
 PRIOR FILING DATE: 1997-03-11  
 PRIOR APPLICATION NUMBER: PC7/US95/14344  
 PRIOR FILING DATE: 1995-10-25  
 PRIOR APPLICATION NUMBER: 07/332,312  
 PRIOR FILING DATE: 1994-10-31  
 NUMBER OF SEQ ID NOS: 74  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 55  
 LENGTH: 312  
 TYPE: PRT  
 ORGANISM: Mus musculus

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RESULT 14
US-09-798-584-1
; Sequence 1, Application US/09798584
; Patent No. US20020102676A1
; GENERAL INFORMATION:
; APPLICANT: Mu, David
; APPLICANT: Powers, Scott
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: KCNB A NO. US20020102676A1 Potassium Channel Protein
; FILE REFERENCE: 018781-00401.00S
; CURRENT APPLICATION NUMBER: US/09/798-584
; CURRENT FILING DATE: 2001-03-03
; PRIOR APPLICATION NUMBER: US 60/186,951
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentNet Ver. 2.1
; SEQ ID NO 1
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human KCNB (Potassium Channel expressed in Breast)
US-09-798-584-1

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TITLE OF INVENTION: NOVEL TWIK-6, TWIK-7, IC3927, TWIK-8, IC47611, IC7615, HNMDA-1, TWIK-9, alpha<sub>2</sub>delta-4, 54414, AND 53763 MOLECULES  
TITLE OF INVENTION: AND USES THEREFOR

Search completed: July 13, 2005, 09:07:02  
Job time : 87.5115 secs

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(c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 13, 2005, 08:10:49 ; Search time 25.273 Seconds  
(without alignments)

1163.760 Million cell updates/sec

Title: US-09-503-089A-5  
Perfect score: 2042  
Sequence: 1 MKRQNRVRLALIVCTFTYLL.....STGHSLSTFRGLMKRRSSV 394

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

## Database :

Issued\_Patents\_AA.\*  
1: /cggn2\_6/ptodata/1/iaa/5A\_COMB.pep:  
2: /cggn2\_6/ptodata/1/iaa/5B\_COMB.pep:  
3: /cggn2\_6/ptodata/1/iaa/6A\_COMB.pep:  
4: /cggn2\_6/ptodata/1/iaa/6B\_COMB.pep:  
5: /cggn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:  
6: /cggn2\_6/ptodata/1/iaa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	2042	100.0	394	3	US-09-144-914-4	Sequence 4, Appli
2	1819	89.1	405	3	US-09-144-914-5	Sequence 5, Appli
3	1116	54.7	388	4	US-09-949-016-7631	Sequence 7631, AP
4	773	37.9	408	4	US-09-365-842-12	Sequence 12, Appli
5	379	18.6	361	4	US-09-365-842-14	Sequence 14, Appli
6	370	370	3	US-09-144-914-8	Sequence 8, Appli	
7	369	18.1	411	3	US-09-236-080-6	Sequence 6, Appli
8	363	17.8	411	3	US-09-236-080-2	Sequence 2, Appli
9	363	17.8	411	3	US-09-336-643A-83	Sequence 83, Appli
10	349.5	17.1	538	4	US-09-949-016-7001	Sequence 7001, AP
11	349.5	17.1	558	4	US-09-949-016-7368	Sequence 7368, AP
12	329.5	16.1	393	4	US-09-432-470-2	Sequence 2, Appli
13	329.5	16.1	393	4	US-09-432-470-4	Sequence 4, Appli
14	329.5	16.1	419	4	US-09-949-016-6913	Sequence 6913, AP
15	329.5	16.1	440	4	US-09-949-016-7809	Sequence 7809, AP
16	320.5	15.7	336	3	US-08-799-816-2	Sequence 2, Appli
17	320.5	15.7	336	3	US-09-144-914-2	Sequence 2, Appli
18	319	15.6	499	4	US-09-561-763-2	Sequence 2, Appli
19	319	15.6	499	4	US-09-411-367B-2	Sequence 2, Appli
20	312	15.3	146	4	US-09-362-842-69	Sequence 69, Appli
21	312	15.3	146	4	US-09-270-767-31685	Sequence 31685, A
22	295.5	14.5	313	3	US-09-316-643A-81	Sequence 81, Appli
23	295.5	14.5	313	4	US-09-561-763-8	Sequence 8, Appli
24	295.5	14.5	313	4	US-09-432-470-8	Sequence 8, Appli
25	294.5	14.4	332	4	US-09-561-765-5	Sequence 5, Appli
26	294.5	14.4	332	4	US-09-411-367B-5	Sequence 5, Appli
27	278.5	13.6	995	4	US-09-362-842-2	Sequence 2, Appli

## ALIGNMENTS

RESULT 1  
US-09-144-914-4  
; Sequence 4, Application US/09144914  
; Patent No. 630855  
; GENERAL INFORMATION:  
; APPLICANT: Duprat, Fabrice  
; APPLICANT: Lebage, Florian  
; APPLICANT: Lazdunski, Michel  
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING  
; FILE REFERENCE: 989\_6705CIP  
; CURRENT APPLICATION NUMBER: US/09-144-914  
; EARLIER APPLICATION NUMBER: 08/749, 816  
; EARLIER FILING DATE: 1998-09-01  
; EARLIER FILING DATE: 1996-11-15  
; EARLIER APPLICATION NUMBER: 60/095, 234  
; EARLIER FILING DATE: 1998-08-04  
; EARLIER APPLICATION NUMBER: FR 95/01565  
; EARLIER FILING DATE: 1996-02-08  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 4  
; LENGTH: 394  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: TASK  
US-09-144-914-4  
Query Match 100.0%; Score 2042; DB 3;  
Best Local Similarity 100.0%; Pred. No. 7.8e-217;  
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MGRQVTLALIVCTFYLLGAATFPEAESPTELERQLRQLRARNLQSQGYE 60  
1 MGRQVTLALIVCTFYLLGAATFPEAESPTELERQLRQLRARNLQSQGYE 60  
61 ELERVYVLRLKPHKAGYQWRFAGSFYFAITVITITGYGAAPSTDGGKVFCMRYALIGIPL 120  
61 ELERVYVLRLKPHKAGYQWRFAGSFYFAITVITITGYGAAPSTDGGKVFCMRYALIGIPL 120  
121 TLVMFQSLGERINTVYLHRAKGLGMRAVDVSHANVVLIGFSCISTLCIGAAFSH 180  
121 TLVMFQSLGERINTVYLHRAKGLGMRAVDVSHANVVLIGFSCISTLCIGAAFSH 180  
181 YEHWTFFQAYTCFIFTTICFGDYLQKDOALOTPOQTYAFTITVIGFLN 240  
181 YEHWTFFQAYTCFIFTTICFGDYLQKDOALOTPOQTYAFTITVIGFLN 240

RESULT 2  
 US-09-144-914-5  
 ; Sequence 5, Application US/09144914  
 ; Patent No. 6309855  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Duprat, Fabrice  
 ; APPLICANT: Lesage, Florian  
 ; APPLICANT: Pinc, Michel  
 ; APPLICANT: Lazdunski, Michel  
 ; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING  
 ; TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS  
 ; FILE REFERENCE: 989.6705CIP  
 ; CURRENT FILING DATE: 1998-09-01  
 ; EARLIER APPLICATION NUMBER: 08/749, 816  
 ; EARLIER FILING DATE: 1996-11-15  
 ; EARLIER APPLICATION NUMBER: 60/095, 234  
 ; EARLIER FILING DATE: 1998-08-04  
 ; EARLIER APPLICATION NUMBER: FR 96/01565  
 ; EARLIER FILING DATE: 1996-02-08  
 ; NUMBER OF SEQ ID NOS: 24  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; LENGTH: 405  
 ; TYPE: PRT  
 ; ORGANISM: Murine  
 ; FEATURE: TASK  
 ; OTHER INFORMATION: TASK  
 ; US-09-144-914-5

Query Match 89.1%; Score 1819; DB 3; Length 405;  
 Best Local Similarity 88.1%; Pred. No. 3.6e-192; Gaps 2;  
 Matches 357; Conservative 9; Mismatches 25; Indels 14;

Db 241 LRVRLPGERINTVRYLLHRAKGGLMHRADYSMANNVLIGFVSCISTLIGAAFSYEH 183  
 Db 121 MFOSLGERINTVRYLLHRAKGGLMHRADYSMANNVLIGFVSCISTLIGAAFSYER 180  
 Db 184 WTEFOQAYYCFITLTIGFGDYVALQDQALOTPOVYAFSPVYILTGTVIGAFNLVV 243  
 Db 181 WTEFOQAYYCFITLTIGFGDYVALQDQALOTPOVYAFSPVYILTGTVIGAFNLVV 240

RESULT 3  
 US-09-949-016-7631  
 ; Sequence 7631, Application US/09949016  
 ; Patent No. 6812339  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VENTER, J. Craig et al.  
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: CL001307  
 ; CURRENT APPLICATION NUMBER: US/09/949, 016  
 ; CURRENT FILING DATE: 2000-04-14  
 ; PRIORITY NUMBER: 60/241,755  
 ; PRIOR FILING DATE: 2000-10-20  
 ; PRIORITY APPLICATION NUMBER: 60/237,768  
 ; PRIOR FILING DATE: 2000-10-03  
 ; PRIORITY APPLICATION NUMBER: 60/231,498  
 ; PRIOR FILING DATE: 2000-09-08  
 ; NUMBER OF SEQ ID NOS: 207012  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO: 7631  
 ; LENGTH: 388  
 ; TYPE: PRT  
 ; ORGANISM: Human  
 ; US-09-949-016-7631

Query Match 54.7%; Score 1116; DB 4; Length 388;  
 Best Local Similarity 59.0%; Pred. No. 1.7e-114;  
 Matches 233; Conservative 44; Mismatches 96; Indels 22; Gaps 5;

Db 15 MKRQNVRTLSLIVCFITLYLVGAADFALDESEPELIERORLELRQOELRLARYNLSOGGYE 60  
 Db 75 QLELTQLQSEPHRGQWKEPGASPFAITVTTIGYHAAPSTDGSKVFCMFYALIGIPL 120  
 Db 121 TLVMPGSLGERINTVRYLLHRAKGGLMHRADYSMANNVLIGFVSCISTLIGAAFSYEH 180  
 Db 135 TLVMPGSLGERMTNTVRYLLKRIKCCGMNTDVSMENMVTFGFCMGTLIGAAFSQ 194  
 Qy 1 MKRQNYRTLALIVCFITLYLVGAADFALDESEPELIERORLELRQOELRLARYNLSOGGYE 60  
 Qy 61 ELERVYVRLRKPHKAGQWKRAGSEYFAITVTTIGYHAAPSTDGSKVFCMFYALIGIPL 120  
 Qy 75 QLELTQLQSEPHRGQWKEPGASPFAITVTTIGYHAAPSTDGSKVFCMFYALIGIPL 134  
 Qy 121 YEHWTQFQAYYYCFITLTIGFGDYVALQDQALOTPOVYAFSPVYILTGTVIGAFNL 240  
 Db 195 CBEWSFHAYYYCFITLTIGFGDYVALQDQALOTPOVYAFSPVYILTGTVIGAFNL 254  
 Qy 241 IYVLERMMDNAEDDEKDAEHLALITRNGQAGGGGGSAHTTDTASSTAAGGGFRNVI 300  
 Db 255 LVVLRLTMSNEDERDAEEBASL-----AGNRNSMVIHPEERPPS-----RPRY 300  
 Qy 301 -AEVLFQSMCSCLWYKSRKQYSPMIIPRDLSTSDTCTVEQSIISSPSGGGRYSDTPSR 359  
 Db 301 KADVPDLOQSVCSCTCYRSQD--YGGRSVAQONSFSAKLAPHYFHSISYKIEBISPLTK 357  
 Qy 360 RCLCGAPRSAISSVSTGLHSLSTFGLMRKRSV 394  
 Db 358 NSLFP-----SPISIISPGHLHSFTDHORLMKRKRSV 388

RESULT 4  
 US-09-362-842-12  
 ; Sequence 12, Application US/09362842  
 ; Patent No. 6511824  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Buchman et al.  
 ; TITLE OF INVENTION: NUCLEIC ACIDS AND POLYPEPTIDES OF INVERTEBRATE TWIK  
 ; FILE REFERENCE: 7326-104  
 ; CURRENT APPLICATION NUMBER: US/09/362, 842  
 ; CURRENT FILING DATE: 1999-07-28  
 ; PRIORITY APPLICATION NUMBER: 09/270, 767

Qy 244 LRPMTNNAEDECRDAEHLALITRNGQAGGGG-----GSSAHTTDTASSTA--- 291  
 Db 244 LRPMTNNAEDECRDAEHLALITRNGQAGGGG-----GSSAHTTDTASSTA--- 291  
 Qy 292 -GGGGPRNVAEVLHQSMCSCLWYKSRKQYSPMIIPRDLSTSDTCTVEQSIISSPSGG 349  
 Db 301 GVGGSGRNVAEVLHQSMCSCLWYKSRKQYSPMIIPRDLSTSDTCTVEHSIISSPSGG 360  
 Qy 350 GGRYSDTPSRRCICSGAPRSAISSVSTGLHSLSTFGLMRKRSV 394

PRIOR FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO: 12  
; LENGTH: 408  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
US-09-362-842-12

Query Match Score 773; DB 4; Length 408;  
Best Local Similarity 43.6%; Pred. No 1..5e-6;  
Matches 164; Conservative 66; Mismatches 82; Indels 64; Gaps 8;

Qy 1 MKRNVRITALIVCFTTYLVGAAYFVDALESEPELIERQRQLRQQELRQARYNLSQGCVB 60  
Db 1 MKQNVRITISLIVCFTTYLVGAAYFVDALESEPELIERQRQLRQQELRQARYNLSQEDPK 60  
Qy 61 ELERVVLRLKPHKAGYQWRPAGSFYFAATVTTTGYGHAPSTCGKVPCMFYALLGFL 120  
Db 61 VMETVVLKSESHKAGQWKTGTGAFYATTWLTIGVGHSTPSTVGKLUFTMCVAIVGFL 120

Qy 121 TLVNFQSGLERINTIVLRLLHARKKGRRADYSMANNAVLIGFSCISTLCLC1-GAAAF 178  
Db 121 GLVMFQSIGERVNRLSSTYTKAVRSSLCKRTVAEVDLICV--VTTLSSLTIGGARF 178

Qy 179 SHYBHWTFFQAYYCFCITLTTIGFDYVALQDQALOTQPOQYVAFSFYVILTGFLTVIGAF 238  
Db 179 SKFEGWSYFSDVYYCFITLTTIGFDYVALQDQALOTQPOQYVAFSFYVILTGFLTVIGAF 238

Qy 239 LNLYVLFRTMNAEDEKRD-EHLR-----LTRNGAGGGGGSAHTDTA 285  
Db 239 LNLYVLFRTMNAEDEKRD-EHLR-----LTRNGAGGGGGSAHTDTA 285

Qy 286 SSTAAGGGFRNYYAEVTFHQSREK--.320  
Db 298 -----NISSMCSCHCITCLNGNRHKSSNLEKNDNAENQKLRSQFT 338

Qy 321 -LQYSIPLIP-RDLS 334  
Db 339 HIRHLPVEVPMQDLN 354

RESULT 5  
US-09-362-842-14  
; Sequence 14, Application US/09362842  
; GENERAL INFORMATION:  
; APPLICANT: Buchman et al.  
; TITLE OF INVENTION: CHANNELS AND POLYPEPTIDES OF INVERTEBRATE TWIK  
; FILE REFERENCE: 7326-104  
; CURRENT FILING DATE: 1999-07-28  
; PRIOR APPLICATION NUMBER: US/09/362,842  
; PRIOR FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO: 14  
; LENGTH: 361  
; TYPE: PRT  
; ORGANISM: Leptinotarsa decemlineata  
US-09-362-842-14

Query Match Score 379; DB 4; Length 361;  
Best Local Similarity 32.4%; Pred. No. 4..6e-33;  
Matches 110; Conservative 52; Mismatches 113; Indels 64; Gaps 13;

Qy 1 MKRNVRITALIVCFTTYLVGAAYFVDALESEPELIERQRQLRQQELRQARYNLSQGCVB 59  
Db 39 MEKTSFRFSIYLKPHKAGV-----QWRFAGSFYFAITVTTTGYGHAPSTDGGCVF 109  
Qy 60 ELERVVLRLKPHKAGV-----QWRFAGSFYFAITVTTTGYGHAPSTDGGCVF 109

Db 99 EEL--IVEVTRANRGSALENATESEPWNWSFGQSFFFFASTVITITGYGHVTPLSRNGKLF 156  
110 CMFVALLGPLTLMPQSGLERINTLVLRRAKKGIG-----MRADVSNANMVLI 162  
157 CMFVAVGGLPLTVLMSLVERLLIPTWLLQWLNLSKGLHYQPURITYVHLAVLVL 216  
163 GFFPSCTISTCIGAFAFSHYE-HMTFFQAYYYCFCITLTTIGFDYVALQDQALOT-QPOY 220  
217 VPF----LILLPAIAFASLEPEWYLDLSLYXCFSLSTLGGLD1--PGDSAHQPYRPLY 269

Db 221 VAFFSVYILTGLTVIGAFINLVV-----IRFMVNAEDEKRD-AEHALLTRNGQAGG 272  
270 KIMTCYLCPLGITIM--MFTLTVYDIPOLNLGLFTTSBSEK-----VRASSGP 319  
273 G---GGGSAHTTITASSTAAGGGFRNYYAEVTLHFQS 308  
320 GLQYGAGFSPHNEB-----NTHRQVVRVRS 344

RESULT 6  
US-09-144-914-8  
; Sequence 8, Application US/09144914  
; Patent No. 6309055  
; GENERAL INFORMATION:  
; APPLICANT: Duprat, Fabrice  
; APPLICANT: Leage, Florian  
; APPLICANT: Pink, Michel  
; APPLICANT: Lazdunski, Michel  
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING  
; TITLE INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS  
; FILE REFERENCE: 989\_6705CIP  
; CURRENT APPLICATION NUMBER: US/09/144, 914  
; CURRENT FILING DATE: 1998-09-01  
; EARLIER APPLICATION NUMBER: 08/749, 816  
; EARLIER FILING DATE: 1996-11-15  
; EARLIER APPLICATION NUMBER: 60/095, 234  
; EARLIER FILING DATE: 1998-08-04  
; EARLIER APPLICATION NUMBER: FR 96/01565  
; EARLIER FILING DATE: 1996-02-08  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 8  
; LENGTH: 370  
; TYPE: PRT  
; ORGANISM: Murine  
; FEATURE:  
; OTHER INFORMATION: TREK-1  
US-09-144-914-8

Query Match Score 370; DB 3; Length 370;  
Best local Similarity 31.6%; Pred. No. 4..7e-32;  
Matches 93; Conservative 57; Mismatches 102; Indels 42; Gaps 9;

Qy 1 MKRNVRITALIVCFTTYLVGAAYFVDALESEPELIERQRQLRQQELRQARYNLSQGCVB 60  
Db 42 MKRNVRITSCLFLV--VVLIGAVKALEQPQEISORTIVQKQTFAQHACVNS--T 97

Qy 61 ELEVRLR-KPHAGV-----QWRFAGSFYFAITVTTTGYHAAPSTDGGCV 108  
Db 98 ELDLIOQQVAATNAGITPLGNNSNQSHWDLGSFFPAGTVITITFGNISPTBEGGKI 157

Qy 109 FCMFYALIGIPLIPLMFQSLGERINTLVLRRAKKGIGMRRAD-----VSM 156  
Db 158 FCTIYALIIGIPLIPLMFQSLGERINTLVLRRAKKGIGMRRAD-----GRGIARKEBDTFLKWNVSQTKRI 208

Qy 157 ANVFLIGFSCISTLCIGAFAFSHYE-HMTFFQAYYYCFCITLTTIGFDYVALQDQALOT 216  
Db 209 ISTIIFLFGCVLFVALPVIKHEGNSALDAYTIVVFLTTIGFDYVAGGSDF-IEY 266

Qy 217 QPQVAFSPVYILGLTGVAFPLV-----VLRDMTNAEDEKRD-AEHALLTRN 267

Db 267 LDFPKPVVWFWLWGLAYPAAVLSMIGDWLRVISKKTKEEVGEFRHAAEWTAN 320

**RESULT 7**  
 US-09-236-080-6  
 Sequence 6, Application US/09236080  
 Patent No. 6242217  
 GENERAL INFORMATION:  
 APPLICANT: Helen Meadows  
 TITLE OF INVENTION: No. 6242217e1 Compounds  
 FILE REFERENCE: GP3 0031  
 CURRENT APPLICATION NUMBER: US/09/236, 080  
 CURRENT FILING DATE: 1999-01-25  
 NUMBER OF SEQ ID NOS: 6  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 SEQ ID NO: 6  
 LENGTH: 411  
 TYPE: PRT  
 ORGANISM: Mus musculus  
 US-09-236-080-6

Query Match 18.1%: Score 369; DB 3; Length 411;  
 Best Local Similarity 31.6%; Pred. No. 7.e-32;  
 Matches 93; Conservative 57; Mismatches 102; Indels 42; Gaps 9;

Qy 1 MKRQNVTIALIVCTFTYLGVAAVEDSEPELIERQRLEHQERARYNLQSOGYE 60  
 Db 42 MKWKTSTIFLVV-VLYLIGTGRAVPALEQPEISORTTRIVIQKQFIAHCVNS-T 97  
 Qy 61 ELERVVRL-KPHKAGV-----QWRFAGSFYFAITVITIGYHAAPSTDGGKV 108  
 Db 98 ELDELIQIVAAINAGTIPLENSSNQVSHMDLGSSFFPAGTVITIGYGNISPRTEGGKI 157  
 Qy 109 FCMFYALGIPLTMFQSLGERINTLVRLHRAKKGLMRRAD-----VSM 156  
 Db 158 FCTIYALGIPDFTFLVVSQTKIRI 208  
 Qy 157 ANMLIGFSCSITLCIGAAAFSHYEMTFEQAYYYCFITLTIGFDDVALQDQALQT 216  
 Db 209 ISTIIFLFGCVLFLVPAVTKHIGEWSALDAIYFVTTIGFDDYVAGGS-D-IEY 266  
 Qy 217 QPOYVAFSFVYLTGTLVIGAFLNV--VLRPMTNNAEDEKRD-AEHRALLTRN 267  
 Db 267 LDFYKPVVWFILVGLAYFAAVLSMIGWLVRISKTKTEEVEFRAHAETWTAN 320

Query Match 17.8%: Score 363; DB 3; Length 411;  
 Best Local Similarity 31.0%; Pred. No. 3.e-31;  
 Matches 91; Conservative 59; Mismatches 102; Indels 42; Gaps 9;

Qy 1 MKRQNVTIALIVCTFTYLGVAAVEDSEPELIERQRLEHQERARYNLQSOGYE 60  
 Db 42 MKWKTSTIFLVV-VLYLIGTGRAVPALEQPEISORTTRIVIQKQFISOCVNS-T 97  
 Qy 61 ELERVVRL-KPHKAGV-----QWRFAGSFYFAITVITIGYHAAPSTDGGKV 108  
 Db 98 ELDELIQIVAAINAGTIPLENSSNQVSHMDLGSSFFPAGTVITIGYGNISPRTEGGKI 157  
 Qy 109 FCMFYALGIPLTMFQSLGERINTLVRLHRAKKGLMRRAD-----VSM 156  
 Db 158 FCTIYALGIPDFTFLVVSQTKIRI 208  
 Qy 157 ANMLIGFSCSITLCIGAAAFSHYEMTFEQAYYYCFITLTIGFDDVALQDQALQT 216  
 Db 209 ISTIIFLFGCVLFLVPAVTKHIGEWSALDAIYFVTTIGFDDYVAGGS-D-IEY 266  
 Qy 217 QPOYVAFSFVYLTGTLVIGAFLNV--VLRPMTNNAEDEKRD-AEHRALLTRN 267  
 Db 267 LDFYKPVVWFILVGLAYFAAVLSMIGWLVRISKTKTEEVEFRAHAETWTAN 320

RESULT 8  
 US-09-236-080-2  
 Sequence 2, Application US/09236080  
 Patent No. 6242217  
 GENERAL INFORMATION:  
 APPLICANT: Conrad Chapman  
 TITLE OF INVENTION: No. 6242217e1 Compounds  
 FILE REFERENCE: GP0031  
 CURRENT APPLICATION NUMBER: US/09/236, 080  
 CURRENT FILING DATE: 1999-01-25  
 NUMBER OF SEQ ID NOS: 6  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 SEQ ID NO: 2  
 LENGTH: 411  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-236-080-2

Query Match 17.8%: Score 363; DB 3; Length 411;  
 Best Local Similarity 31.0%; Pred. No. 3.e-31;  
 Matches 91; Conservative 59; Mismatches 102; Indels 42; Gaps 9;

Qy 1 MKRQNVTIALIVCTFTYLGVAAVEDSEPELIERQRLEHQERARYNLQSOGYE 60  
 Db 42 MKWKTSTIFLVV-VLYLIGTGRAVPALEQPEISORTTRIVIQKQFISOCVNS-T 97  
 Qy 61 ELERVVRL-KPHKAGV-----QWRFAGSFYFAITVITIGYHAAPSTDGGKV 108

GENERAL INFORMATION:  
 APPLICANT: VENTER, J. Craig et al.  
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 FILE REFERENCE: CLO001307  
 CURRENT APPLICATION NUMBER: US/09/949, 016  
 PRIOR APPLICATION NUMBER: 2000-04-14  
 PRIOR FILING DATE: 2000-10-20  
 PRIOR APPLICATION NUMBER: 60/241, 755  
 PRIOR FILING DATE: 2000-10-20  
 PRIOR APPLICATION NUMBER: 60/237, 768  
 PRIOR FILING DATE: 2000-10-03  
 PRIOR APPLICATION NUMBER: 60/231, 498  
 PRIOR FILING DATE: 2000-09-08  
 NUMBER OF SEQ ID NOS: 207012  
 SOFTWARE: FastSEQ For Windows Version 4.0  
 SEQ ID NO: 7001  
 LENGTH: 538  
 TYPE: PRT  
 ORGANISM: Human  
 US-09-949-016-7001

Query Match Score 349.5; DB 4; Length 538;  
 Best Local Similarity 32.8%; Pred. No. 1.5e-29;  
 Matches 95; Conservative 53; Mismatches 109; Indels 33; Gaps 10;  
 Result 12

US-09-432-470-2

Qy 1 MKRQNVRTIALIVCTFTYLGVAAVEDALESEPELIERQRLELRQE-LRARYNLSQCGY 59  
 Db 67 MKWKTV--VAIFVUVVVVLTGGLVRALEQPPESSONTIALEKAELRDIYCVSP--- 121  
 Qy 60 EELERVVLR-LKPHKAGV-----QWRFAGSFYFAITVTTTGYHAPSTDGK 107  
 Db 122 QELETLQHALDADNAGSPIGNSNNSSHWDLGSAFPAGVTTTGYGNATAPSTEGK 181  
 Qy 108 VFCMFYALGIPITLVMFQSLGERINTLVRLHRAKKGMRADYSMANN-----VLI 162  
 Db 182 IFCLYAFGIPLEGFLAGIDOLGTGFKSSTARVEK-VFRKKQVSQTKRVISTILF 239  
 Qy 163 GFPSCISTICIGAAFSHYEHWTFFOAYYYCFITLTIGFDYVALQKDQALOTQPYVA 222  
 Db 240 ILAGCIVVTGTLTVIGAFANLV--VLFRTMNAEDEKRD----AEHRALLT 265  
 Qy 223 FSFVYIILTGLTVIGAFANLV--VLFRTMNAEDEKRD----AEHRALLT 265  
 Db 299 LVNFWILGLAYFAVLSMIGDWRLVSKTKTKEEVGETKAHAEWKAVNT 348

Query Match Score 349.5; DB 4; Length 538;  
 Best Local Similarity 32.8%; Pred. No. 1.5e-29;  
 Matches 95; Conservative 53; Mismatches 109; Indels 33; Gaps 10;  
 Result 12

US-09-432-470-2

Qy 1 MKRQNVRTIALIVCTFTYLGVAAVEDALESEPE-LIERQRLELRQE-LRARYNLSQCGY 59  
 Db 67 MKWKTV--VAIFVUVVVVLTGGLVRALEQPPESSONTIALEKAELRDIYCVSP--- 121  
 Qy 60 EELERVVLR-LKPHKAGV-----QWRFAGSFYFAITVTTTGYHAPSTDGK 107  
 Db 122 QELETLQHALDADNAGSPIGNSNNSSHWDLGSAFPAGVTTTGYGNATAPSTEGK 181  
 Qy 108 VFCMFYALGIPITLVMFQSLGERINTLVRLHRAKKGMRADYSMANN-----VLI 162  
 Db 182 IFCLYAFGIPLEGFLAGIDOLGTGFKSSTARVEK-VFRKKQVSQTKRVISTILF 239  
 Qy 163 GFPSCISTICIGAAFSHYEHWTFFOAYYYCFITLTIGFDYVALQKDQALOTQPYVA 222  
 Db 240 ILAGCIVVTGTLTVIGAFANLV--VLFRTMNAEDEKRD----AEHRALLT 265  
 Qy 223 FSFVYIILTGLTVIGAFANLV--VLFRTMNAEDEKRD----AEHRALLT 265  
 Db 299 LVNFWILGLAYFAVLSMIGDWRLVSKTKTKEEVGETKAHAEWKAVNT 348

Query Match Score 329.5; DB 4; Length 393;  
 Best Local Similarity 31.0%; Pred. No. 1.5e-27;  
 Matches 98; Conservative 43; Mismatches 112; Indels 63; Gaps 8;

Qy 9 LALIVCPTTYLGVAAVDALESEPE-LIERQRLELRQE-LRARYNLSQCGY 56  
 Db 7 LAULALVLYVSGALYVRALEQPPESSONTIALEKAELRDIYCVSP--- 163  
 Qy 57 --GGYBLLERVVLR-LKPHKAGVQWRFAGSFYFAITVTTTGYHAPSTDGKVFMCY 113  
 Db 67 DALGGADPETSNSHSAA-WDLGSAPPFGTITIGVNLRTDAGLFCFY 123  
 Qy 114 AIIGIPITLVMFQSLGERINTLVRLHRAKKGMRAD-----VSMANMVLG 163  
 Db 124 ALVGPPLFGLLAVGDRGLSSLRH-----GIGHEAIFLKWHVPPBLVRLSAMPL 176  
 Qy 164 FFSCISTICIGAAFSHYEHWTFFOAYYYCFITLTIGFDYVALQKDQALOTQPYVA 223  
 Db 177 LIGCIFWLFVLTPTFVCFYMEDWSKLEALYFVIVTLLTVGFDFVAGADER--QDSPAYQPL 234  
 Qy 224 SFVYIILT-----LTVIGAFLNVLVLFMTMINADEKRAEHLTRNGGGGG 276  
 Db 235 VWFWILGLAYFAVLSMIGDWRLVSKTKTKEEVGETKAHAEWKAVNT 275

Query Match Score 349.5; DB 4; Length 558;  
 Best Local Similarity 32.8%; Pred. No. 1.6e-29;

Qy 277 GSAAHTTDTASSTAAG 292  
 Db 276 ASNTGTVTARVTOAG 291

US-09-949-016-7368  
 Sequence 7368, Application US/09949016  
 Patent No. 6812339  
 GENERAL INFORMATION:  
 APPLICANT: VENTER, J. Craig et al.  
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 FILE REFERENCE: CLO001307  
 CURRENT APPLICATION NUMBER: US/09/949, 016  
 CURRENT FILING DATE: 2000-04-14  
 PRIOR APPLICATION NUMBER: 60/241, 755  
 PRIOR FILING DATE: 2000-10-20  
 PRIOR APPLICATION NUMBER: 60/237, 768  
 PRIOR FILING DATE: 2000-10-03  
 PRIOR APPLICATION NUMBER: 60/231, 498  
 PRIOR FILING DATE: 2000-09-08  
 NUMBER OF SEQ ID NOS: 207012  
 SOFTWARE: FastSEQ For Windows Version 4.0  
 SEQ ID NO: 7368  
 LENGTH: 558  
 TYPE: PRT  
 ORGANISM: Human  
 US-09-949-016-7368

RESULT 13  
US-09-432-470-4  
Sequence 4, Application US/09432470  
GENERAL INFORMATION:  
APPLICANT: David Malcolm Duckworth  
TITLE OF INVENTION: NOVEL COMPOUNDS  
FILE REFERENCE: GP-30190  
CURRENT FILING DATE: 1999-11-03  
EARLIER APPLICATION NUMBER: UK 9923668.9  
EARLIER FILING DATE: 1999-10-07  
EARLIER APPLICATION NUMBER: UK 9824048.4  
EARLIER FILING DATE: 1998-11-03  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: FastSEQ for Windows Version 3.0  
SEQ ID NO 4  
LENGTH: 393  
TYPE: PRT  
ORGANISM: HOMO SAPIENS  
US-09-432-470-4

Query Match 16.1%; Score 329.5; DB 4; Length 419;  
Best Local Similarity 31.0%; Pred. No. 1.7e-27;  
Matches 98; Conservative 43; Mismatches 112; Indels 63; Gaps 8;  
US-09-949-016-6913

Qy 9 LALIVCTFTYLGVAAVDALESEPE-LIERQRLRQELRARNYLNLSQ----- 56  
Db 33 LALLALVLLVLYSGALVFRALEQPHEQQAQRELGEYREKFLRAHPCVSQDQLGLLKEVA 92  
Qy 57 ---GGYEBELERVRLKPKHAGQWRFAGSFYFAATVITIGYGHAAAPSTDGGKVFCMFY 113  
Db 93 DALGGGADPETNSTNSHHSA --WDLGSAFFSFTGTTTGYGNVALRTDAGRFLCFY 149  
Qy 114 ALLGIPLTLMFQSLSGERINTLVRLHRAKKGGMRRAD----- VSMAANMVLIG 163  
Db 150 ALVGIPPLFGILLLAGQDRGSSLRH-----GIGHIEAFLKWHVWPPLEVRLVLSMLFL 202  
Qy 164 FFSCISTLCLGAAAFHYEWTFQAYYYCPTLTGFDYVALQKDQALQTQPOVYAF 223  
Db 203 LIGCLLFLVLTPTFVCFYMEDWSKLEAFYFVITLTGFDYVAGADPR--QDSPAYQPL 260  
Qy 224 SFVYLTG-----LTVIGAFLNLVLRMTMNAEDEKRDAEHRLTRNGAQAGGGGG 276  
Db 261 VWFWILLGLAYFASVLTIGNWLRRVVSRR-----TRAEMGLTQAQ 301

Query Match 16.1%; Score 329.5; DB 4; Length 393;  
Best Local Similarity 31.0%; Pred. No. 1.5e-27;  
Matches 98; Conservative 43; Mismatches 112; Indels 63; Gaps 8;  
US-09-432-470-4

Qy 9 LALIVCTFTYLGVAAVDALESEPE-LIERQRLRQELRARNYLNLSQ----- 56  
Db 7 LALLALVLLVLYSGALVFRALEQPHEQQAQRELGEYREKFLRAHPCVSQDQLGLLKEVA 66  
Qy 57 ---GGYEBELERVRLKPKHAGQWRFAGSFYFAATVITIGYGHAAAPSTDGGKVFCMFY 113  
Db 67 DALGGGADPETNSTNSHHSA --WDLGSAFFSFTGTTTGYGNVALRTDAGRFLCFY 123  
Qy 114 ALLGIPLTLMFQSLSGERINTLVRLHRAKKGGMRRAD----- VSMAANMVLIG 163  
Db 124 ALVGIPPLFGILLLAGQDRGSSLRH-----GIGHIEAFLKWHVWPPLEVRLVLSMLFL 176  
Qy 164 FFSCISTLCLGAAAFHYEWTFQAYYYCPTLTGFDYVALQKDQALQTQPOVYAF 223  
Db 177 LIGCLLFLVLTPTFVCFYMEDWSKLEAFYFVITLTGFDYVAGADPR--QDSPAYQPL 234  
Qy 224 SFVYLTG-----LTVIGAFLNLVVRMTMNAEDEKRDAEHRLTRNGAQAGGGGG 276  
Db 235 VWFWILLGLAYFASVLTIGNWLRRVVSRR-----TRAEMGLTQAQ 275  
Qy 277 GSAHTTDASSTAAG 292  
Db 276 ASWTGTVTARVQRAG 291

RESULT 14  
US-09-949-016-6913  
Sequence 6913, Application US/09949016  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949.016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/12339  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 7809  
LENGTH: 440  
TYPE: PRT  
ORGANISM: Human  
US-09-949-016-6913

Query Match 16.1%; Score 329.5; DB 4; Length 440;  
Best Local Similarity 31.0%; Pred. No. 1.8e-27;  
Matches 98; Conservative 43; Mismatches 112; Indels 63; Gaps 8;  
US-09-949-016-6913

Qy 9 LALIVCTFTYLGVAAVDALESEPE-LIERQRLRQELRARNYLNLSQ----- 56  
Db 54 LALLALVLLVLYSGALVFRALEQPHEQQAQRELGEYREKFLRAHPCVSQDQLGLLKEVA 113  
Qy 57 ---GGYEBELERVRLKPKHAGQWRFAGSFYFAATVITIGYGHAAAPSTDGGKVFCMFY 113  
Db 114 DALGGGADPETNSTNSHHSA --WDLGSAFFSFTGTTTGYGNVALRTDAGRFLCFY 170  
Qy 114 ALLGIPLTLMFQSLSGERINTLVRLHRAKKGGMRRAD----- VSMAANMVLIG 163

Db	171	ALVGIPLEGILLAGVGDBLGSSLRH-----GIGHIEAIFLKWKWVPPELYVLSAMPLFL	223
Qy	164	FFSCISTLICIGARAFSHYHTEFFQAYTYCFTTLTIGFGDVALQKDQALOTOPQYVAF	223
Db	224	LIGCLLPFLPTPFLPTFVFCYMEDWSKLEATYFVIVLTTVFGDVAGADR--DDSPAVQPL	281
Qy	224	SFYIILTG-----LTWIGAFILNLYVURFMMAEDEKRDAEHRLALLTRNGQAGGGGG	276
Db	282	VNFWMILGLAYFAVSVLTTIGNWLRRVSSR-----TRAEMGGJTAQA	322
Qy	277	GSAHTTDASSTAAG	292
Db	323	ASWTGTVTARVTORAG	338

Search completed: July 13, 2005, 08:47:06  
Job time : 26.273 secs

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Copyright (c) 1993 - 2005 Compugen Ltd.	GenCore version 5.1.6	Ade08315 Novel pro Add62910 Human NOV Aau19473 Human tra Aao14193 Human tra Add127190 Human TRI Abu60891 Human G-P Aav94426 Human h-T Aay94425 Human h-T Aas67777 Human meC Aag78406 Amino aci Aae38597 Human pot Ade51550 Hematolog Add151639 Human 123 Add127936 Human TWI Add44894 Polypepti Aau04571 Human G-P Abu60872 Human G-P Aay3647 A mechan Aae16598 Human TWI Abg02731 Novel hum		
OM protein - protein search, using sw model				
Run on:	July 13, 2005, 07:58:54 ; Search time 101.398 Seconds (without alignments)			
	1567.669 Million cell updates/sec			
Title:	US-09-503-089A-4			
Perfect score:	2090			
Sequence:	1 MAAPDLDPKSAAQNSKPRL,.....LNGLTPHCAGEDIAVIENMK 411			
Scoring table:	BLOSUM62			
	Gapop 10.0 , Gapext 0.5			
Searched:	2105692 seqB, 386760381 residues			
Total number of hits satisfying chosen parameters:	2105692			
Minimum DB seq length:	0			
Maximum DB seq length:	2000000000			
Post-processing: Minimum Match 0\$ Maximum Match 100\$		RESULT 1 AAE10342		
Listing First 45 summaries		XX standard; protein; 411 AA. AAE10342;		
Database :	A_Geneseq_16Dec04: 1: geneseqP19808:/* 2: geneseqP19908:/* 3: geneseqP20008:/* 4: geneseqP20016:/* 5: geneseqP20026:/* 6: geneseqP20038:/* 7: geneseqP20038:/* 8: geneseqP20048:/*	AC XX DT 10-DEC-2001 (first entry) XX DE Murine TREK-1 potassium channel protein. XX KW Murine; potassium channel protein; TREK-1; anaesthetic; analgesia; KW amnesia. XX OS Mus musculus. XX PN WO2000047738-A2. XX PD 17-AUG-2000. XX PF 11-FEB-2000; 2000WO-1B000226. XX PR 12-FEB-1999; 99US-0111977P. PR 11-FEB-2000; 2000US-00503089. XX (CNRS ) CNRS CENT NAT RECH SCI. XX PI Lazdunski M, Honore E, Lesage F, Rometry G, Patel AJ; XX DR WP; 2000-549146/50. DR N-DSDB; AAD17497. XX PT Novel nucleic acid encoding a TREK-1 potassium channel protein for transfected cells to be used to identify compounds with anesthetic properties.		
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.				
SUMMARIES				
Result No.	Query	Description		
	Match	Length		
	DB	ID		
1	2090	100.0	411 3 AAE10342	AAE10342 Murine TR
2	2094	99.7	411 2 AAY28497	AAY28497 Mouse h-T
3	2044	97.8	411 2 AAY3133	AAY3133 Human pot
4	2044	97.8	411 2 AAY28496	AAY28496 h-TREK1 P
5	2044	97.8	411 4 AAB5044	AAB5044 Human TRE
6	2044	97.8	411 7 ADP0586	ADP0586 Human GPC
7	2044	97.8	411 8 ADQ76698	ADQ76698 Human two
8	2041	97.7	411 3 AAE10341	AAE10341 Human TRE
9	2038	97.5	422 7 ADP0575	ADP0575 Human GPC
10	2033	97.3	411 3 AAE16597	AAE16597 Human TWI
11	2011	96.2	426 4 AAU07618	AAU07618 Human pot
12	2007	96.0	426 4 AAU07622	AAU07622 Human pot
13	2006	96.0	426 4 AAU07623	AAU07623 Human pot
14	2003	95.8	426 4 AAU07625	AAU07625 Human pot
15	2002	95.8	426 4 AAU07624	AAU07624 Human pot
16	1864	89.7	370 2 AAY30648	AAY30648 A mechan
17	1620.5	77.5	337 6 ABR41487	ABR41487 Human DTR
18	1251.5	59.9	538 5 AAB47930	AAB47930 Human TRE
19	1251.5	59.9	538 5 AAE16596	AAE16596 Human TWI
20	1251.5	59.9	538 5 ABP63333	ABP63333 Human pol
21	1251.5	59.9	543 5 AAE21804	AAE21804 Human TRE
22	1251.5	59.9	543 5 AAU81354	AAU81354 Novel hum
23	1251.5	59.9	543 5 ABB83542	ABB83542 Hypothala
24	1251.5	59.9	543 6 ADA05746	ADA05746 Human NOV
25	1251.5	59.9		Sequence 411 AA;
		SQ		

Query Match	100.0%	Score 2090; DB 3;	Length 411;	
Best Local Similarity	100.0%	Pred. No. 3.5e-218;		
Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Qy 1 MAAPDLQPKSAQNSKPRLSFSKPTVLASRVESD SAINMKWKTSTIPLVWVLYLII 60				
Db 1 MAAPDLQPKSAQNSKPRLSFSKPTVLASRVESD SAINMKWKTSTIPLVWVLYLII 60				
Qy 61 GAAVEKAQEQPIQSORTTIVIQQTETIAQACVNSTDELIQQIVAAINAGIIPIGNS 120				
Db 61 GAAVEKAQEQPIQSORTTIVIQQTETIAQACVNSTDELIQQIVAAINAGIIPIGNS 120				
Qy 121 SNQVSHWLGSSEFFAGTVITITGFGNISPREGGKFCITIVALLGIPLGFLLAGYDQ 180				
Db 121 SNQVSHWLGSSEFFAGTVITITGFGNISPREGGKFCITIVALLGIPLGFLLAGYDQ 180				
Qy 181 LGTIFGKQIAKVEDTFIKWNVSOTKIRIISTIIFLFGCVLFVALPAVIFKHIEGWSALD 240				
Db 181 LGTIFGKQIAKVEDTFIKWNVSOTKIRIISTIIFLFGCVLFVALPAVIFKHIEGWSALD 240				
Qy 241 AIVFVVTIITTGDFDYAGGSDEIYIARYKPVWMEFLVGLAYFAVLSMIGDWLRVIS 300				
Db 241 AIVFVVTIITTGDFDYAGGSDEIYIARYKPVWMEFLVGLAYFAVLSMIGDWLRVIS 300				
Qy 301 KITKEEVGFRAAENTANVTAPEKFTRRSVEITDKFQATSVKRLSAAELAGHNQ 360				
Db 301 KITKEEVGFRAAENTANVTAPEKFTRRSVEITDKFQATSVKRLSAAELAGHNQ 360				
Qy 361 ELTPCRRTLSVNHLTSEREVLPPLLKAESIYLNGLTPHCAEDIAVENMK 411				
Db 361 ELTPCRRTLSVNHLTSEREVLPPLLKAESIYLNGLTPHCAEDIAVENMK 411				
RESULT 2				
AY28497				
ID AAY28497	standard, protein;	411 AA.		
XX AAY28497;				
XX 12-OCT-1999	(first entry)			
DE Mouse h-TREK1 polypeptide.				
XX h-TREK1; two pore potassium channel; inflammatory disease;				
XX chromosome 1q32.				
XX OS musculus.				
XX PN WO9937762-A1.				
XX PD 29-JUL-1999.				
XX PF 02-DEC-1998;	98WO-EP0078805.			
XX PR 27-JAN-1998;	98EP-00300570.			
XX PR 09-OCT-1998;	98GB-00022135.			
XX PA (SMIK ) SMITHKLINE BEECHAM PLC.				
XX PI Meadows HJ, Chapman CG;				
XX DR 1999-469126/39.				
XX N-PSDB; AA200040.				
XX New two pore potassium channel used for, e.g. treatment of cancer,				
XX PR pulmonary, cardiovascular and inflammatory diseases.				
XX PS Claim 3; Page 26; 44PP; English.				
XX CC This sequence is the mouse h-TREK1 polypeptide, encoded by the h-TREK1 polynucleotide AA200040. h-TREK1 is a two pore potassium channel. The polynucleotide sequence of h-TREK1 can be used to diagnose a disease or susceptibility to a disease related to expression or activity of h-TREK-1.				
XX CC				
XX CC diseases including cancer, pulmonary, cardiovascular, and inflammatory diseases, pain, psychiatric disorders including depression and schizophrenia, neurodegenerative diseases including Alzheimer's, stroke, and head trauma and neurological disorders including migraine				
XX XX Sequence 411 AA;				
Query Match	99.7%	Score 2084;	DB 2;	Length 411;
Best Local Similarity	99.8%;	Pred. No. 1.6e-217;		
Matches 410; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
Qy 1 MAAPDLQPKSAQNSKPRLSFSKPTVLASRVESD SAINMKWKTSTIPLVWVLYLII 60				
Db 1 MAAPDLQPKSAQNSKPRLSFSKPTVLASRVESD SAINMKWKTSTIPLVWVLYLII 60				
Qy 61 GAAVEKAQEQPIQSORTTIVIQQTETIAQACVNSTDELIQQIVAAINAGIIPIGNS 120				
Db 61 GAAVEKAQEQPIQSORTTIVIQQTETIAQACVNSTDELIQQIVAAINAGIIPIGNS 120				
Qy 121 SNQVSHWLGSSEFFAGTVITITGFGNISPREGGKFCITIVALLGIPLGFLLAGYDQ 180				
Db 121 SNQVSHWLGSSEFFAGTVITITGFGNISPREGGKFCITIVALLGIPLGFLLAGYDQ 180				
Qy 181 LGTIFGKQIAKVEDTFIKWNVSOTKIRIISTIIFLFGCVLFVALPAVIFKHIEGWSALD 240				
Db 181 LGTIFGKQIAKVEDTFIKWNVSOTKIRIISTIIFLFGCVLFVALPAVIFKHIEGWSALD 240				
Qy 241 AIVFVVTIITTGDFDYAGGSDEIYIARYKPVWMEFLVGLAYFAVLSMIGDWLRVIS 300				
Db 241 AIVFVVTIITTGDFDYAGGSDEIYIARYKPVWMEFLVGLAYFAVLSMIGDWLRVIS 300				
Qy 301 KITKEEVGFRAAENTANVTAPEKFTRRSVEITDKFQATSVKRLSAAELAGHNQ 360				
Db 301 KITKEEVGFRAAENTANVTAPEKFTRRSVEITDKFQATSVKRLSAAELAGHNQ 360				
Qy 361 ELTPCRRTLSVNHLTSEREVLPPLLKAESIYLNGLTPHCAEDIAVENMK 411				
Db 361 ELTPCRRTLSVNHLTSEREVLPPLLKAESIYLNGLTPHCAEDIAVENMK 411				
RESULT 3				
AAY34133				
ID AAY34133	standard, protein;	411 AA.		
XX AAY34133;				
AC AC				
XX DT 30-NOV-1999	(first entry)			
XX DE Human potassium channel K+Hn0v59.				
XX KW Potassium channel; ataxia; arrhythmia; epilepsy; Bartter's syndrome; cardiovascular disorder; CNS disorder; renal disorder.				
XX OS Homo sapiens.				
XX PN WO943696-A1.				
XX PD 02-SEP-1999.				
XX PF 22-FEB-1999;	99WO-US003826.			
XX PR 25-FEB-1998;	98US-007667P.			
XX PR 07-AUG-1998;	98US-0095816P.			
XX PR 19-JAN-1999;	99US-0116448P.			
XX PA (AXYS-) AXYS PHARM INC.				
XX PI Miller AP, Curran ME, Hu P, Rutter M, Wang J;				
XX CC				
CC DR WPI; 1999-527591/44.				
CC DR N-PSDB; AAZ11915.				

New nucleic acids encoding mammalian K<sup>+</sup>Hnok potassium channel proteins, useful for the diagnosis and treatment of episodic ataxia with myokymia, cardiac arrhythmia, epilepsy and Bartter's syndrome.

Claim 3: Page 104-105; 112PP; English.

This sequence represents the human K<sup>+</sup>Hnok59 potassium channel. K<sup>+</sup>Hnok proteins have a high degree of homology to known potassium channels and may be alpha subunits, which form the functional channel, or accessory subunits that act to modulate the channel activity. K<sup>+</sup>Hnok59 is a 4 transmembrane domain, 2 pore domain potassium channel. The gene is located on chromosome 19, determined via PCR chromosomal localisation using primers AAZ19193 and AAZ1940. K<sup>+</sup>Hnok cDNAs were isolated by extension of expressed sequence tags (ESTs) which were related but not identical to known human potassium channels. Potential polymorphisms detected as sequence variants between multiple independent clones. Potassium channels have critical roles in various cell types and biochemical pathways. Defective potassium channels are known to cause four human diseases: episodic ataxia with myokymia, cardiac arrhythmia (long QT syndrome); epilepsy; and Bartter's syndrome. As potassium channels are critical components of virtually all cells, it is likely that abnormal potassium channels are also implicated in certain renal, cardiovascular and central nervous system (CNS) disorders. Nucleotides encoding K<sup>+</sup>Hnok proteins may be used for identifying homologous or related proteins and the DNA sequences encoding them. They may be used to produce compositions that modulate the expression and function of the K<sup>+</sup>Hnok protein and in studying the biochemical pathways associated with it. They may also be used for the recombinant production of K<sup>+</sup>Hnok protein in fermentation cultures. Additionally, such nucleotides may be used in gene therapy protocols for the treatment of diseases associated with abnormal potassium channels.

Sequence 411 AA;						
	Query Match	Score	DB 2-	Length	411;	
	Best Local Similarity	97.0%	Pred. No.	3..5e-2.13;		
	Matches	96.4%;	Mismatches	4;		
	Local Similarity	96.4%;	Indels	0;		
	Matches	396;	Caps	0;		
1	MAAPDLDPKSAONSKPRLSFSSKPTVTLASRVESDSAINTMKWKTSTIFLVVYLYLII	60				
1	MAAPDLDPKSAONSKPRLSFSSKPTVTLASRVESDSAINTMKWKTSTIFLVVYLYLII	60				
61	GAAVFKALEQPOEISQRRTIVIQKQTFLIAQHACVNSTELDELQIQTVAIAAIGIIPLGNS	120				
61	GATVFKALEQPHESQRRTIVIQKQTFSQHSCVNSTELDELQIQTVAIAAIGIIPGNT	120				
121	SNQSYHWDLGSSPFPAFTVTTIGFQNTSPRTGGK1FCIIYALLG1PLFGLFPLASGVGDQ	180				
121	SNQSYHWDLGSSPFPAFTVTTIGFQNTSPRTGGK1FCIIYALLG1PLFGLFPLASGVGDQ	180				
181	LGTIFGKG1AKVEDTFIKMNVSQTKIRISTI1FILFGCVLFVALPAVIFRHEIGNSALD	240				
181	LGTIFGKG1AKVEDTFIKMNVSQTKIRISTI1FILFGCVLFVALPAVIFRHEIGNSALD	240				
241	AIVFVITLTIGFDDYAGGSDEYLDFYKPVWFWLVLGIAFYAAVLSMIGDWLRVIS	300				
241	AIVFVITLTIGFDDYAGGSDEYLDFYKPVWFWLVLGIAFYAAVLSMIGDWLRVIS	300				
301	KKTK1KEVGEFRHAEMTANVTAEEFKETRRLSVE1YDKFQRATSVKRKLSAELAGNHQ	360				
301	KKTK1KEVGEFRHAEMTANVTAEEFKETRRLSVE1YDKFQRATSVKRKLSAELAGNHQ	360				
361	ELTPCRTLSVNHTJTSEREVLPPLKAEISYINGLPHCAGEDIAVENMK	411				
361	ELTPCRTLSVNHTJTSEREVLPPLKAEISYINGLPHCAGEDIAVENMK	411				

Db	361 ELTPCRRTLSVNHLTSEBDVLPPLLKTESIYLNGLTPHCAEGBIAVENIK 411	Qy	181 LGTIGFGKGIAKVEDPIKNNVSGOTKIRIISTIIFLFGCVLFVALPAVIFKHIEGNSALD 240
RESULT 5		Db	181 LGTIGFGKGIAKVEDPIKNNVSGOTKIRIISTIIFLFGCVLFVALPAVIFKHIEGNSALD 240
AAB50044		Qy	241 AIVFVITLTIGFDYVAGGSIDIELDFYKPVVVFILVGLAYAAVLSMIGDWLRVIS 300
ID AAB50044 standard; protein; 411 AA.		Db	241 AIVFVITLTIGFDYVAGGSIDIELDFYKPVVVFILVGLAYAAVLSMIGDWLRVIS 300
XX		Qy	301 KKTKEEVGEPRHAEAETWTANNTAETKETTRRLSVPILDYKFORATSYKRKLSAELAGNHNO 360
AC AAB50044;		Db	301 KKTKEEVGEPRHAEAETWTANNTAETKETTRRLSVPILDYKFORATSYKRKLSAELAGNHNO 360
XX		Qy	361 ELTPCRRTLSVNHLTSEREVPLPLKASETYINGLTPHCAGEDIAVIVENIK 411
DT 19-MAR-2001 (first entry)		Db	361 ELTPCRRTLSVNHLTSEREVPLPLKASETYINGLTPHCAGEDIAVIVENIK 411
DB Human TREK.		Qy	RESULT 6
XX		Db	ADP03586 standard; protein; 411 AA.
KW 2P domain potassium channel; resting membrane potential;		XX	ADP03586;
KW neuronal excitability; neurotransmitter release modulation; epilepsy;		XX	AC ADP03586;
KW neurological disorder; sleep-related disorder; cognitive dysfunction;		XX	XX
KW attention deficit disorder; addiction; anxiety; phobia;		XX	29-JUL-2004 (first entry)
KW Parkinson's chorea; Huntington's chorea; cerebral palsy; incontinence;		XX	XX
KW erectile dysfunction; alopecia.		XX	Human GPCR potassium channel, subfamily K, member 2 protein.
XX		XX	XX
OS Homo sapiens.		XX	GPCR, G-protein coupled receptor; neuroprotective; nootropic;
PN WO2000072863-A2.		XX	tranquilliser; antimigraine; neuroleptic; antimanic; antidepressant;
XX		XX	anticonvulsant; antiparkinsonian; cytostatic; cardiotonic; hypotensive;
PD 07-DEC-2000.		XX	antiangiinal; analgesic; anorectic; anti-HIV; antiasthmatic; osteopathic;
PF 01-JUN-2000; 2000WO-GB002107.		XX	uropathic; antiluler; antiallergic; cell cycle regulation; neurological;
XX		XX	severe mental retardation; dyskinesia; brain; spinal cord; affective;
PR 01-JUN-1999; 99GB-00012733.		XX	KW neoplastic; cardiovascular; immunological; immune; endocrinian; growth;
XX		XX	KW eating; HIV infection; cancer; metabolic; pituitary;
PA (SMIK ) SMITHKLINE BEECHAM PLC.		XX	KW chromosome identification; gene therapy; human; receptor;
XX		XX	KW potassium channel subfamily K member 2.
PI Hervieu GJ, Meadows HJ, Randall AD;		OS Homo sapiens.	
XX		XX	
WPI; 2001-080422/09.		XX	WO2003062393-A2.
DR N-PSDB; AAC90412.		XX	
XX		XX	31-JUL-2003.
PT Use of human TREK1 polypeptides encoding them and		XX	22-JAN-2003; 2003WO-US001911.
PT modulators of h-TREK1 polypeptides for treating epilepsy, sleep-related		XX	
PT disorders, addiction and dyskinesias including Parkinson's and		XX	22-JAN-2002; 2002US-0350724P.
PT Huntington's chorea.		XX	(BRIM ) BRISTOL-MYERS SQUIBB CO.
PS Claim 7; Page 29; 35PP; English.		XX	
XX		XX	PI Ramanathan CS, Gopal S, Mintier G, Feder JN;
CC The present sequence is human TREK1 (h-TREK1). h-TREK1 is a member of the		XX	XX
CC 2P domain potassium channel family of proteins which play a part in the		XX	WPI; 2003-618283/58.
CC control of resting membrane potential. Modulation of these channels will		XX	
CC therefore affect neuronal excitability, thereby leading to a modulation		XX	PT New nucleic acid molecule encoding a human G-protein coupled receptor,
CC of neurotransmitter release and activity of neuronal networks. Such		XX	PT useful for diagnosing, preventing or treating diseases involving the
CC modulation therefore may be useful for the treatment of certain		XX	PT receptor, e.g., Parkinson's disease, dementia, asthma, hypertension or
CC neurological conditions such as epilepsy, sleep-related disorders,		XX	PT cancer.
CC cognitive dysfunction, attention deficit disorder, addiction,		XX	XX
CC anxiety, phobia, Parkinson's and Huntington's chorea, cerebral palsy,		XX	Example 1; SEQ ID NO 31; 224pp; English.
CC incontinence, erectile dysfunction or alopecia.		XX	
XX		PS	
Query Match 97.8%; Score 2044; DB 4; Length 411;			
Best Local Similarity 96.4%; Pred. No. 3.5e-2.3;			
Matches 396; Conservative 11; Mismatches 4; Indels 0; Gaps 0;			
Qy 1 MAAPDLILPKSAQNSKERLFSQSKPVLASRVESDPAINYMKWKTIVSTTFLVVVLYII 60			
Db 1 MAAPDLILPKSAQNSKERLFSQSKPVLASRVESDPAINYMKWKTIVSTTFLVVVLYII 60			
Qy 61 GAAVFKALEQPOETISORTIVIQQTFAQHACVNSTDELIQQIVAINAGIIPGNS 120			
Db 61 GAAVFKALEQPOETISORTIVIQQTFAQHACVNSTDELIQQIVAINAGIIPGNS 120			
Qy 121 SNQVSHWLQGSSPFAGTTTGFGNSPRTEGGKLFICITYALLGIPLGFLLAGVGDQ 180			
Db 121 SNQVSHWLQGSSPFAGTTTGFGNSPRTEGGKLFICITYALLGIPLGFLLAGVGDQ 180			

CC disorders, neoplastic disorders, cardiovascular disorders, immunological  
 CC disorders, immune-related disorders, endocrinial diseases, growth  
 CC disorders, eating disorders, HIV infection, cancers, metabolic disorders  
 CC and pituitary disorders. Furthermore, the polynucleotide may be used in  
 CC chromosome identification, in identifying organisms from minute  
 CC biological samples, in gene therapy or as a molecular weight marker. The  
 CC current sequence is that of a human GPCR (G-protein coupled receptor)  
 CC protein of the invention which was used for homology purposes.

XX Sequence 411 AA;

Query Match 97.8%; Score 2044; DB 7; Length 411;  
 Best Local Similarity 96.4%; Pred. No. 3.5e-213;  
 Matches 396; Conservative 11; Mismatches 4; Indels 0; Gaps 0;  
 Qy 1 MAAPDLDPKSAQNSKPRLSFSSKPTLASRVSSTDINMKWKTSTIFLVVLYLII 60  
 Db 1 MAAPDLDPKSAQNSKPRLSFSSKPTLASRVSSTDINMKWKTSTIFLVVLYLII 60  
 Qy .61 GAAVFKALEQPOETSORTTIVIQKQTFLAQHACVNSTELDELQIQAIVANAGLIPLGNS 120  
 Db 61 GATVFKALEQPHISORTTIVIQKQTFSQHSCVNSTELDELQIQAIVANAGLIPLGNT 120  
 Qy 121 SNOQSHWDLGSSFPAGTVTTIGFGNISPRTEGGKFCITIALLGLPFGFLAGYDQ 180  
 Db 121 SNQISHWDLGSSFPAGTVTTIGFGNISPRTEGGKFCITIALLGLPFGFLAGYDQ 180  
 Qy 181 LGTIFGKGIAKVEFTFIKWNSQTKIRIISTIIFLRCPVLFALPAVTFKHLEGNSALD 240  
 Db 181 LGTIFGKGIAKVEFTFIKWNSQTKIRIISTIIFLRCPVLFALPAVTFKHLEGNSALD 240  
 Qy 241 AIVFVVIITLTIGFGDYTAGGSDEIYLDFYKPVWNEFLVGLAYFAAVLSMIGDWLRVIS 300  
 Db 241 AIVFVVIITLTIGFGDYTAGGSDEIYLDFYKPVWNEFLVGLAYFAAVLSMIGDWLRVIS 300  
 Qy 301 KCTKEEVGSEFRHAAEWTANVTAEFTKTRRLSVEITDKPQATSVRKLSAELAGNHQ 360  
 Db 301 KCTKEEVGSEFRHAAEWTANVTAEFTKTRRLSVEITDKPQATSVRKLSAELAGNHQ 360  
 Qy 361 ELTPCRRTLSVNHLTSEBPPLKASITYINGLTPHCAEGDIAVENMK 411  
 Db 361 ELTPCRRTLSVNHLTSEBPPLKASITYINGLTPHCAEGDIAVENIK 411

## RESULT 7

ADQ76638 ID ADQ76638 standard; protein; 411 AA.  
 XX AC ADQ76638;  
 XX DT 07-OCT-2004 (first entry)  
 XX DE Human two pore domain potassium channel TREK-1.  
 XX KW sleep; two pore domain potassium channel; sedative; hypnotic;  
 KW human.  
 XX OS Homo sapiens.  
 XX PN WO200458325-A2.  
 XX PD 15-JUL-2004.  
 XX PP 23-DEC-2003; 2003WO-US040913.  
 XX PR 23-DEC-2002; 2004US-0436201P.  
 XX PA (WISC ) WISCONSIN ALUMNI RES FOUND.

XX PI Tononi G, Cirelli C;

XX DR WPI; 2004-534024/51.

GENBANK; NM014217.

XX PT Identifying a Drosophila mutant fly with a no rebound, short sleep and/or  
 PT no sleep deprivation resistant phenotype, for identifying sleep-related  
 PT molecular targets, comprises recording sleep quantity of the mutant fly.  
 XX PS Claim 12; SEQ ID NO 2; 83pp; English.  
 XX The present sequence is that of the human two pore domain K<sup>+</sup> channel TREK-1. In rats, TREK-1 is highly expressed in much of the brain and is inhibited by protein kinase C and protein kinase C mediated phosphorylation. It is activated by volatile general anaesthetics and is expressed at high levels in the brain of sleep animals. Based on these criteria and on experimental results, it is hypothesized that TREK-1 is a key mediator of sleep (when open) and waking (when closed). The invention provides methods for identifying a sleep- or wakefulness-promoting compound based on the compound's ability to modulate two pore domain K<sup>+</sup> channels such as TREK-1. It also provides screening methods for isolating short sleep, no rebound and sleep deprivation resistant Drosophila mutants useful for identifying sleep-related molecular targets.  
 XX Sequence 411 AA;  
 Query Match 97.8%; Score 2044; DB 8; Length 411;  
 Best Local Similarity 96.4%; Pred. No. 3.5e-213;  
 Matches 396; Conservative 11; Mismatches 4; Indels 0; Gaps 0;  
 Qy 1 MAAPDLDPKSAQNSKPRLSFSSKPTLASRVSSTDINMKWKTSTIFLVVLYLII 60  
 Db 1 MAAPDLDPKSAQNSKPRLSFSSKPTLASRVSSTDINMKWKTSTIFLVVLYLII 60  
 Qy 61 GAAVFKALEQPOETSORTTIVIQKQTFLAQHACVNSTELDELQIQAIVANAGLIPLGNS 120  
 Db 61 GATVFKALEQPHISORTTIVIQKQTFSQHSCVNSTELDELQIQAIVANAGLIPLGNT 120  
 Qy 181 SNOQSHWDLGSSFPAGTVTTIGFGNISPRTEGGKFCITIALLGLPFGFLAGYDQ 180  
 Db 181 SNOQSHWDLGSSFPAGTVTTIGFGNISPRTEGGKFCITIALLGLPFGFLAGYDQ 180  
 Qy 241 AIVFVVIITLTIGFGDYAGGSDEIYLDFYKPVWNEFLVGLAYFAAVLSMIGDWLRVIS 300  
 Db 241 AIVFVVIITLTIGFGDYAGGSDEIYLDFYKPVWNEFLVGLAYFAAVLSMIGDWLRVIS 300  
 Qy 301 KCTKEEVGSEFRHAAEWTANVTAEFTKTRRLSVEITDKPQATSVRKLSAELAGNHQ 360  
 Db 301 KCTKEEVGSEFRHAAEWTANVTAEFTKTRRLSVEITDKPQATSVRKLSAELAGNHQ 360  
 Qy 361 ELTPCRRTLSVNHLTSEBPPLKASITYINGLTPHCAEGDIAVENMK 411  
 Db 361 ELTPCRRTLSVNHLTSEBPPLKASITYINGLTPHCAEGDIAVENIK 411

RESULT 8  
 AAB10341 ID AAB10341 standard; protein; 411 AA.  
 XX AC AAB10341;  
 XX DT 10-DEC-2001 (first entry)  
 XX DE Human TREK-1 potassium channel protein.  
 XX KW Human; potassium channel protein; TREK-1; anaesthetic; analgesia;  
 KW amnesia.  
 XX OS Homo sapiens.  
 XX PN WO20047738-A2.  
 XX DR 17-AUG-2000.

XX 11-FEB-2000; 2000WO-IB000226.  
 PP GPCR; G-protein coupled receptor; neuroprotective; nocropic;  
 XX tranquilliser; antimigraine; neuroleptic; antimanic; antidepressant;  
 XX anticonvulsant; antiparkinsonian; cytotatic; cardiant; hypotensive;  
 PR 12-FEB-1999; 99US-0119727P.  
 PR 11-FEB-2000; 2000US-00503089.  
 XX (CNRS ) CNRS CENT NAT RECH SCI .  
 PA Lazdunski M, Honore E, Lesage F, Romay G, Patel AJ;  
 XX DR; WPI: 2000-549146/50.  
 XX DR; AAd17498.  
 XX Novel nucleic acid encoding a TREK-1 potassium channel protein for  
 PT transfecting cells to be used to identify compounds with anaesthetic  
 PT properties.  
 XX Claim 3: Page 28; 39pp; English.  
 CC The invention relates to human and mouse TREK-1 potassium channel  
 CC proteins and their corresponding DNA molecules. TREK-1 nucleic acid is  
 CC useful for transfecting cells to induce expression of the TREK-1  
 CC potassium channel protein. These cells are then used in assays to  
 CC identify compounds which have anaesthetic properties, producing a safe,  
 CC reversible state of unconsciousness with concurrent amnesia and analgesia  
 CC in a mammal upon inhalation. The present sequence is human TREK-1  
 CC potassium channel protein  
 XX Sequence 411 AA;  
 SQ Query Match 97.7%; Score 2041; DB 3; Length 411;  
 Best Local Similarity 96.1%; Pred. No. 7.5e-213;  
 Matches 395; Conservative 12; Mismatches 4; Indels 0; Gaps 0;  
 Qy 1 MAAPDLDPKSAQNSKPRLSRSPSKPTVLASRVESDSTAINYMKWVTVSTIPLVVVLYLII 60  
 Db 1 MAAPDLDPKSAQNSKPRLSRSPSKPTVLASRVESDSTAINYMKWVTVSTIPLVVVLYLII 60  
 Qy 61 GRAVFKALEQPBIQSPTTIVQKQPIQHACNNTDELIQVIAANAGIPLIGNS 120  
 Db 61 GATVFKALEQPBIQSPTTIVQKQPIQHACNNTDELIQVIAANAGIPLIGNT 120  
 Qy 121 SNOVSHWDLGSSRFAGTTTGFNNISPRTEGGKLFCIYALIGILPFLGQLLAGVGDQ 180  
 Db 121 SNOVSHWDLGSSRFAGTTTGFNNISPRTEGGKLFCIYALIGILPFLGQLLAGVGDQ 180  
 Qy 181 LGTIFGKGIAKYBDTFTIKWNVSQTKRKRISTIITFLFGCVLFVALPAVIFKHIEGWSALD 240  
 Db 181 LGTIFGKGIAKYBDTFTIKWNVSQTKRKRISTIITFLFGCVLFVALPAVIFKHIEGWSALD 240  
 Qy 241 AYIFVWLTITLGFDYAGGSDEIVLDFYKTFRRSVEYDKFDRATSVKRLSAELAGNNHQ 300  
 Db 241 AYIFVWLTITLGFDYAGGSDEIVLDFYKTFRRSVEYDKFDRATSVKRLSAELAGNNHQ 300  
 Qy 301 KICPKEEVGFRAHAAETVANTAEFKTRERRSVEYDKFDRATSVKRLSAELAGNNHQ 360  
 Db 301 KICPKEEVGFRAHAAETVANTAEFKTRERRSVEYDKFDRATSVKRLSAELAGNNHQ 360  
 XX Sequence 422 AA;  
 Qy 361 ELTPCRRFLSVNHLTSREVLPLKKAESIYLNGLTPHAGEDIAYTENMK 411  
 Db 361 ELTPCRRFLSVNHLTNERDVLPLKTESIYLNGLTPHAGEDIAYTENIK 411  
 Qy RESULT 9  
 ID ADP03575 standard; protein: 422 AA.  
 XX  
 AC ADP03575;  
 XX DR 29-JUL-2004 (first entry)  
 XX Human GPCR twin pore channel" protein variant "Gene 9" protein.  
 Db 121 SNOVSHWDLGSSRFAGTTTGFNNISPRTEGGKLFCIYALIGILPFLGQLLAGVGDQ 180  
 Db 132 SNOVSHWDLGSSRFAGTTTGFNNISPRTEGGKLFCIYALIGILPFLGQLLAGVGDQ 191

KW GPCR; G-protein coupled receptor; neuroprotective; nocropic;  
 KW tranquilliser; antimigraine; neuroleptic; antimanic; antidepressant;  
 KW anticonvulsant; antiparkinsonian; cytotatic; cardiant; hypotensive;  
 KW antiallergic; analgesic; anorectic; anti-HIV; antiasthmatic; osteopathic;  
 KW uropathic; antiluler; antiulcer; dyskinisia; brain; spinal cord; affective;  
 KW severe mental retardation; dyskinisia; immunological; immune; endocrin; growth;  
 KW neoplastic; cardiovascular; immunological; gene therapy; human; receptor;  
 KW eating; HIV infection; cancer; metabolic; pituitary;  
 KW chromosome identification; gene therapy; human; receptor;  
 KW twin pore channel; potassium channel subfamily K member 2 variant.  
 XX OS Homo sapiens.  
 XX PN WO2003062393-A2.  
 XX PN WO2003062393-A2.  
 XX PD 31-JUL-2003.  
 XX PP 22-JAN-2003; 2003WO-US001911.  
 XX PR 22-JAN-2002; 2002US-0350724P.  
 XX PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 XX PI Ramanathan CS, Godal S, Mintier G, Feder JN;  
 XX WPI: 2003-618283/58.  
 DR N-PBDB; ADP03564.  
 XX DR N-PBDB; ADP03564.  
 XX New nucleic acid molecule encoding a human G-protein coupled receptor,  
 PT useful for diagnosing, preventing or treating diseases involving the  
 PT receptor, e.g. Parkinson's disease, dementia, asthma, hypertension or  
 PT cancer.  
 XX Claim 5: SEQ ID NO 20; 224pp; English.  
 XX PS The invention relates to a novel isolated GPCR (G-protein coupled  
 receptor) nucleic acid molecule. The polynucleotide and polypeptide of  
 CC the invention demonstrate neuroprotective, nootropic, tranquiliser,  
 CC anticonvulsant, analgesic, antihypertensive, antianginal,  
 CC antiparkinsonian, cytotatic, cardiant, hypotensive, anticonvulsant,  
 CC analgesic, anorectic, anti-HIV, antiasthmatic, osteopathic, uropathic,  
 CC antiluler and antiallergic properties. The nucleic acid molecule and  
 CC polypeptide of the invention may be useful in diagnosing, preventing,  
 CC treating or ameliorating a medical condition, such as a disorder related to aberrant  
 CC cell cycle regulation, neurological disorders, severe mental retardation  
 CC and dyskinesias, brain disorders, spinal cord disorders, affective  
 CC disorders, neoplastic disorders, cardiovascular disorders, immunological  
 CC disorders, immune-related disorders, endocrin diseases, growth  
 CC disorders, eating disorders, HIV infection, cancers, metabolic disorders  
 CC and pituitary disorders. Furthermore, the polynucleotide may be used in  
 CC chromosome identification, in identifying organisms from minute  
 CC biological samples, in gene therapy or as a molecular weight marker. The  
 CC current sequence is that of a human GPCR (G-protein coupled receptor)  
 CC protein which was isolated by the method of the invention.  
 XX Sequence 422 AA;  
 Qy Query Match 97.5%; Score 2038; DB 7; Length 422;  
 Best Local Similarity 95.9%; Pred. No. 1.7e-212;  
 Matches 394; Conservative 13; Mismatches 4; Indels 0; Gaps 0;  
 Qy 1 MAAPDLDPKSAQNSKPRLSRSPSKPTVLASRVESDSTAINYMKWVTVSTIPLVVVLYLII 60  
 Db 12 LAAPDLDPKSAQNSKPRLSRSPSKPTVLASRVESDSTAINYMKWVTVSTIPLVVVLYLII 71  
 Qy 61 GRAVFKALEQPBIQSPTTIVQKQPIQHACNNTDELIQVIAANAGIPLIGNS 120  
 Db 72 GATVFKALEQPBIQSPTTIVQKQPIQHACNNTDELIQVIAANAGIPLIGNT 131  
 Qy 121 SNOVSHWDLGSSRFAGTTTGFNNISPRTEGGKLFCIYALIGILPFLGQLLAGVGDQ 180  
 Db 132 SNOVSHWDLGSSRFAGTTTGFNNISPRTEGGKLFCIYALIGILPFLGQLLAGVGDQ 191

Qy	181	LGTIFGKGIAKVEDTEIKNVNSQTKIRLISITIIFLGCGVLFYALPAVIFKHIEGWSALD 240	CC and moderately in testis, brain, colon and small intestine. The mammalian K <sup>+</sup> channel protein is useful in methods for screening various compounds.
Db	192	LGTIFGKGIAKVEDTEIKNVNSQTKIRLISITIIFLGCGVLFYALPAVIFKHIEGWSALD 251	CC In particular, the protein is useful in methods for identifying biologically active compounds with anaesthetic properties. The present sequence is TREK-1 protein used in the invention
Qy	241	AIVFVITLTIGDGYAGGSDEYLDPYKPVWFLVGLAYFAAVLSMIDMLRVIS 300	XX
Db	252	AIVFVITLTIGDGYAGGSDEYLDPYKPVWFLVGLAYFAAVLSMIDMLRVIS 311	XX
Qy	301	KCTKEEVGFEKKAETVNTAFTKEFTRRLSVEIYDFQRATSVKRLSADLAGNINQ 360	Query Match 97.3%; Score 2033; DB 5; Length 411;
Db	312	KCTKEEVGFEKKAETVNTAFTKEFTRRLSVEIYDFQRATSVKRLSADLAGNINQ 371	Best Local Similarity 95.9%; Pred. No. 5.e-212; Mismatches 5; Indels 0; Gaps 0;
Qy	361	ELTPCRRTLSVNHLTSEREVLPPLKAKASIVIYGLTPHCAGEDTAVIFRMK 411	Matches 394; Conservative 12; Gaps 0;
Db	372	ELTPCRRTLSVNHLTSEREVLPPLKAKASIVIYGLTPHCAGEDTAVIFRMK 422	Qy 1 MAAPDLIDPKSAANQSKERLSSFSKPTVLASRVSDAISVNRWKTVSTIFLVVLVLI 60
<b>RESULT 10</b>			
AAE16597		AAE16597 standard; protein; 411 AA.	Db 1 MAAPDLIDPKSAANQSKERLSSFSKPTVLASRVSDAISVNRWKTVSTIFLVVLVLI 60
XX			Qy 61 GAAVFKALEQPOEISORTTIVIQKQTFTAQHACVNSTELDELIQQTVAIAQGIPGNS 120
AC			Db 61 GAAVFKALEQPOEISORTTIVIQKQTFTAQHACVNSTELDELIQQTVAIAQGIPGNS 120
XX			Qy 61 GAAVFKALEQPHISQRTTIVIQKQTFTAQHACVNSTELDELIQQTVAIAQGIPGNS 120
XX			Db 121 SNQVSHNDLGSSPFFASTVTTIGFGNISPRTEGGKIFCIIYALGLIPFGFLAGVGDQ 180
XX			Db 121 SNQVSHNDLGSSPFFASTVTTIGFGNISPRTEGGKIFCIIYALGLIPFGFLAGVGDQ 180
XX			Qy 181 LGTFIYGKGLIAKVEDTPIKWNVSOTKIRLSTITIIFLGCVLFYALPAVIFKHIEGWSALD 240
XX			Db 181 LGTFIYGKGLIAKVEDTPIKWNVSOTKIRLSTITIIFLGCVLFYALPAVIFKHIEGWSALD 240
DE			Qy 241 AIVFVITLTIGDGYAGGSDEYLDFYKPVWFLVGLAYFAAVLSMIDMLRVIS 300
XX			Db 241 AIVFVITLTIGDGYAGGSDEYLDFYKPVWFLVGLAYFAAVLSMIDMLRVIS 300
KW			OS Homo sapiens.
XX			Qy 301 KTKKEEVGEFRAAETVNTAFTKEFTRRLSVEIYDKFORATSVKRKLSAELAGHNQ 360
XX			Db 301 KTKKEEVGEFRAAETVNTAFTKEFTRRLSVEIYDKFORATSVKRKLSAELAGHNQ 360
OS			Qy 361 ELTPCRRTLSVNHTSEREVLPPLKAKASIVIYGLTPHCAGEDTAVIENMK 411
XX			Db 361 ELTPCRRTLSVNHTSEREVLPPLKAKASIVIYGLTPHCAGEDTAVIENMK 411
Key			RESULT 11
FT Region	47. .65	/note= "M1 membrane spanning segment"	AAU07618
FT Domain	127. .150	/note= "P1 pore domain"	ID AAU07618 standard; protein; 426 AA.
FT Region	158. .178	/note= "M2 membrane spanning segment"	XX AAU07618;
FT Region	209. .230	/note= "M3 membrane spanning segment"	XX DT 21-NOV-2001 (first entry)
FT Domain	236. .259	/note= "P2 pore domain"	DB Human potassium ion channel TPKC1 protein.
FT Region	274. .293	/note= "M4 membrane spanning segment"	XX KW Transmembrane potassium ion channel protein; inward potassium flux;
FT	PN WO200200715-A2.		XX KW pest control; membrane potential; pesticide; antihelminthic; nematode;
XX	03-JAN-2002.		XX Insect; TPKC1; human.
PP	27-JUN-2001; 2001WO-IB001436.		XX Homo sapiens.
XX	27-JUN-2000; 2000US-0214559P.		XX WO200161006-A2.
PR	27-JUN-2001; 2001US-00892360.		XX PD 23-AUG-2001.
XX	(CNRS ) CNRS CENT NAT RECH SCI.		XX PR 14-FEB-2001; 2001WO-US004680.
PR	Lazdunski M, Leagee F, Romney G;		XX PR 15-FEB-2000; 2000US-00503849.
XX	WPI ; 2002-139903/18.		XX (BADI ) BASF CORP.
PR	New mammalian K <sup>+</sup> channel protein with two pore domains, for screening various compounds, particularly for identifying biologically active compounds with anaesthetic properties.		XX PA Pausch MH;
PR	The invention relates to a mammalian K <sup>+</sup> channel protein with two pore domains, called TRBK2 (TWIK-Related K <sup>+</sup> Channel). The protein produces currents whose current-voltage relationship is slightly inwardly rectifying in high symmetrical K <sup>+</sup> conditions. TREK2 is a member of the fatty acid-activated and mechanosensitive K <sup>+</sup> channel family. TREK-2 gene located on chromosome 14q31 is abundantly expressed in kidney, pancreas		XX DR WPI ; 2001-516570/59.
PS	Disclosure: Fig 1A; 50pp; English.		XX DR N-PSDB; AAS12169.
XX	CC New polypeptide, a mutant potassium ion channel protein for improving		XX PT

PT inward potassium flux under acidic conditions.  
 XX  
 PS Example 15; Page 45; 131pp; English.

CC The invention relates to a mutant potassium ion channel protein, having a four membrane spanning domains and two pore forming domain. The expression of the mutant protein at the second pore forming domain. The expression of the mutant protein in a cell confers improved inward potassium flux and the ability to grow in the presence of potassium. Mutant proteins and their corresponding polynucleotide sequences can therefore be used to improve inward potassium flux into cells under acidic conditions by modulating the membrane potential using therapeutic agents. The sequences may be used to develop agonists and antagonists of potassium channel proteins in order to control pests such as nematodes and insects. This sequence represents a human transmembrane potassium ion channel protein, TPKC1

XX  
 SQ Sequence 426 AA;

Query Match	96.2%	Score 2011; DB 4; Length 426;
Best Local Similarity	95.1%	Pred. No. 1.5e-209;
Matches	391	Conservative 13; Mismatches 7; Indels 0; Gaps 0;

Qy 1 MAAPDLIDPKSAAQNSKPRLSFSKPTVLASRVEDSDAINMKWKTSTIFLVLVLYLII 60  
 Db 16 VAAPDLIDPKSAAQNSKPRLSFSKPTVLASRVEDSDAINMKWKTSTIFLVLVLYLII 75

Qy 61 GRAVFKALEQPIQSQTIVIQQQTETIAQHACVNSTELDELQIQIVAAINAGIIPLGNS 120  
 Db 76 GATVFKALEQPIEISQTIVIQQQTETISQSCVNSTELDELQIQIVAAINAGIIPLGNT 135

Qy 121 SNQVSHMDLGSSPFPPAGTIVITIGFQNSIPREGGKFCITCYALGIPRLGFLLAGYGDQ 180  
 Db 136 SNQVSHMDLGSSPFPPAGTIVITIGFQNSIPREGGKFCITCYALGIPRLGFLLAGYGDQ 195

Qy 181 LGTIFGKQIAKYEDTFIKWNVSQTKTRISTIIFLGCVLFWALPAVIFKHIEGMNALD 240  
 Db 196 LGTIFGKQIAKYEDTFIKWNVSQTKTRISTIIFLGCVLFWALPAVIFKHIEGMNALD 255

Qy 241 AIVFVWLTITIGFGDYYAGGSDFIILDYKPVVWWFILVGLAYPAVLSMIGDWTRVIS 300  
 Db 256 AIVFVWLTITIGFGDYYAGGSDFIILDYKPVVWWFILVGLAYPAVLSMIGRLRVIS 315

Qy 301 KTKKEEVGEFRHAENTANTAEFKTRRRLSVEITDKFQRATSVKRKLSAELAGHNQ 360  
 Db 316 KTKKEEVGEFRHAENTANTAEFKTRRRLSVEITDKFQRATSVKRKLSAELAGHNQ 375

Qy 361 ELTPCRTLTSVNHLSERVLPLLLKAESIYINGLTPHAGEDIAVLENMK 411  
 Db 376 ELTPCRTLTSVNHLSERVLPLLLTESIYINGLAPHCAGEIAVENIK 426

RESULT 1.2  
 AAU07622 standard; protein: 426 AA.  
 XX  
 AC AAU07622;  
 XX DT 21-NOV-2001 (first entry)  
 XX Human potassium ion channel TPKC1 mutant protein #1.  
 XX Transmembrane potassium ion channel protein; inward potassium flux; pest control; membrane potential; pesticide; antihelminthic; nematode; insect; TPKC1; human; mutant; mutein.  
 XX Homo sapiens.  
 XX  
 FH Location/Qualifiers  
 FT Misc-difference 256  
 /note= "Wild-type Ala replaced by Thr"  
 PT  
 XX  
 PN WO200161006-A2.

RESULT 1.3  
 AAU07623  
 ID AAU07623 standard; protein: 426 AA.  
 XX  
 AC AAU07623;  
 XX DT 21-NOV-2001 (first entry)

PD 23-AUG-2001.  
 XX  
 PP 14-FEB-2001; 2001WO-US004680.  
 XX  
 PR 15-FEB-2000; 2000US-00503849.  
 XX  
 PA (BADI ) BASF CORP.  
 XX  
 PI Pausch MH;  
 XX  
 DR WPI; 2001-536570/59.  
 DR N-PDB; AAS12181.  
 XX  
 PT New polypeptide, a mutant potassium ion channel protein for improving inward potassium flux under acidic conditions.  
 XX  
 PS Claim 37; Page 113-115; 131pp; English.  
 XX  
 CC The invention relates to a mutant potassium ion channel protein, having four membrane spanning domains and two pore forming domains, comprising a mutation at the second pore forming domain. The expression of the mutant protein in a cell confers improved inward potassium flux and the ability to grow in the presence of potassium. Mutant proteins and their corresponding polynucleotide sequences can therefore be used to improve inward potassium flux into cells under acidic conditions by modulating the membrane potential using therapeutic agents. The sequences may be used to develop agonists and antagonists of potassium channel proteins in order to control pests such as nematodes and insects. This sequence represents a human transmembrane potassium ion channel TPKC1 mutant protein  
 XX  
 SQ Sequence 426 AA;

Query Match	96.0%	Score 2007; DB 4; Length 426;
Best Local Similarity	94.9%	Pred. No. 4e-209;
Matches	390	Conservative 13; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MAAPDLIDPKSAAQNSKPRLSFSKPTVLASRVEDSDAINMKWKTSTIFLVLVLYLII 60  
 Db 16 VAAPDLIDPKSAAQNSKPRLSFSKPTVLASRVEDSDAINMKWKTSTIFLVLVLYLII 75

Qy 61 GRAVFKALEQPIEISQTIVIQQQTETISQSCVNSTELDELQIQIVAAINAGIIPLGNS 120  
 Db 76 GATVFKALEQPIEISQTIVIQQQTETISQSCVNSTELDELQIQIVAAINAGIIPLGNT 135

Qy 121 SNQVSHMDLGSSPFPPAGTIVITIGFQNSIPREGGKFCITCYALGIPRLGFLLAGYGDQ 180  
 Db 136 SNQVSHMDLGSSPFPPAGTIVITIGFQNSIPREGGKFCITCYALGIPRLGFLLAGYGDQ 195

Qy 181 LGTIFGKQIAKYEDTFIKWNVSQTKTRISTIIFLGCVLFWALPAVIFKHIEGMNALD 240  
 Db 196 LGTIFGKQIAKYEDTFIKWNVSQTKTRISTIIFLGCVLFWALPAVIFKHIEGMNALD 255

Qy 241 AIVFVWLTITIGFGDYYAGGSDFIILDYKPVVWWFILVGLAYPAVLSMIGDWTRVIS 300  
 Db 256 AIVFVWLTITIGFGDYYAGGSDFIILDYKPVVWWFILVGLAYPAVLSMIGRLRVIS 315

Qy 301 KTKKEEVGEFRHAENTANTAEFKTRRRLSVEITDKFQRATSVKRKLSAELAGHNQ 360  
 Db 316 KTKKEEVGEFRHAENTANTAEFKTRRRLSVEITDKFQRATSVKRKLSAELAGHNQ 375

Qy 361 ELTPCRTLTSVNHLSERVLPLLLKAESIYINGLTPHAGEDIAVLENMK 411  
 Db 376 ELTPCRTLTSVNHLSERVLPLLLTESIYINGLAPHCAGEIAVENIK 426

RESULT 1.2  
 AAU07622 standard; protein: 426 AA.  
 XX  
 AC AAU07622;  
 XX DT 21-NOV-2001 (first entry)  
 XX Human potassium ion channel TPKC1 mutant protein #1.  
 XX Transmembrane potassium ion channel protein; inward potassium flux; pest control; membrane potential; pesticide; antihelminthic; nematode; insect; TPKC1; human; mutant; mutein.  
 XX Homo sapiens.  
 XX  
 FH Location/Qualifiers  
 FT Misc-difference 256  
 /note= "Wild-type Ala replaced by Thr"  
 PT  
 XX  
 PN WO200161006-A2.



				CC used to develop agonists and antagonists of potassium channel proteins in order to control pests such as nematodes and insects. This sequence represents a human transmembrane potassium ion channel TPKC1 mutant protein.
				CC
				CC
				CC
				XX
			SQ Sequence 426 AA;	
			Query Match 95.8%; Score 2002; DB 4; Length 426;	
			Best Local Similarity 94.6%; Pred. No. 1.4e-208; Mismatches 8; Indels 0; Gaps 0;	
			Matches 389; Conservative 14;	
			Qy 1 MAAPDLDPKSAAQNSKPRISFSSKPTVLASRVEEDSDAINNMWKWVSTIFLVVLYLII 60	
			Db 16 VAAPDLDPKSAAQNSKPRISFSTKEPTVLASRVEEDSDTINNMWKWVSTIFLVVLYLII 75	
			Qy 241 AIVFFVITLTIGFDYAGGSDEIYLDFYKEVWWFWILVGLAYFAAVLSMIGDWLRVIS 300	
			Db 256 AIVFFVITLTIGFRDYAGGSDEIYLDFYKEVWWFWILVGLAYFAAVLSMIGRLVRVIS 315	
			Qy 301 KTKKEEVGEFRAAETVNTAEFKTRRRLSVEIYDKEFORATSKRKTLSAELAGHNQ 360	
			Db 316 KTKKEEVGEFRAAETVNTAEFKTRRRLSVEIYDKEFORATSKRKLSAELAGHNQ 375	
			Qy 361 ELTPCRRTLSVNHLSEREVPLKLKEASIVNLPHCAGEDIAVENMK 411	
			Db 376 ELTPCRRTLSVNHLSERDVLPPLKLESTIVNLPHACASEEIAVENIK 426	
		RESULT 15		
	AAU07624	standard; protein; 426 AA.		
	ID	AAU07624		
	XX			
	AC			
	XX			
	DT			
	XX			
	DE			
	Human potassium ion channel TPKC1 mutant protein #3.			
	KW			
	Transmembrane potassium ion channel protein; inward potassium flux; pest control; membrane potential; pesticide; antihelminthic; nematode; insect; TPKC1; human; mutant; mutein.			
	KW			
	XX			
	OS			
	Homo sapiens.			
	XX			
	FH			
	Misc-difference 272			
	FT			
	FT 21-NOV-2001 (First entry)	/note= "Wild-type Tyr replaced by His"		
	XX			
	FT			
	FT Misc-difference 274	/note= "Wild-type Ala replace by Val"		
	XX			
	PN	WO200161006-A2.		
	XX			
	PD			
	XX	23-AUG-2001.		
	PP			
	XX	14-FEB-2001; 2001WO-US004680.		
	PR			
	XX	15-FEB-2000; 2000US-00503849.		
	PA			
	XX	(BADI ) BASF CORP.		
	PI			
	XX	Pausch MH;		
	DR			
	XX	WPI; 2001-536570/59.		
	DR			
	XX	N-PSDB; AAS12183.		
	PT			
	XX	New polypeptide, a mutant potassium ion channel protein for improving inward potassium flux under acidic conditions.		
	XX			
	PS	Claim 37; Page 117-119; 131pp; English.		
	XX	The invention relates to a mutant potassium ion channel protein, having a four membrane spanning domains and two pore forming domains comprising a second pore forming domain. The expression of the mutant protein in a cell confers improved inward potassium flux and the ability to grow in the presence of potassium. Mutant proteins and their corresponding polynucleotide sequences can therefore be used to improve inward potassium flux into cells under acidic conditions by modulating the membrane potential using therapeutic agents. The sequences may be		





Db	244	AIVVVITLTGFDYVAGGS DIE LDYKPVVWFNLLVGLAYFAAVLSMIGDWLRVIS	303	Db	76	GATVKALEQOPQEISORTTIVIQKONFIQAHACVNSTELDELJQIVTAINAGIPLGNN	135	
Qy	301	KTKKEEVGEPRHAEEWVANVIAEKFETRRRLSVEIYKFKRATSVKRLSAELGNHNQ	360	Qy	121	SNQVSHNDLGSEFFFASTVITIGFGNISPRTEGGKPCIIYALLGIPLGFLLAGVGQ	180	
Db	304	KTKKEEVGEPRHAEEWVANVIAEKFETRRRLSVEIYKFKRATSVKRLSAELGNHNQ	363	Db	136	SNQVSHNDLGSEFFPAGTVITIGFGNISPRTEGGKFCITYALLGIPLGFLAGVGQ	195	
Qy	361	ELTPCRRTLSVNHLTSEREVLPPLKAKSIYLNGLTPCAGEDIAVIENMK	411	Qy	181	LGTIFGKIAKVDFTIKWNYSQTKRKLISTIIFLFGCVLFVALPAVIFKIEGWSALD	240	
Db	364	ELTPCRRTLSVNHLTSEREVLPPLKAKSIYLNGLTPCAGEDIAVIENMK	414	Db	196	LGTIFGKIAKVDFTIKWNYSQTKRKLISTIIFLFGCVLFVALPAVIFKIEGWSALD	255	
<b>RESULT 3</b>								
Q92OB6		PRELIMINARY;	PRT;	426 AA.	Qy	241	AIVFVITLTGFDYVAGGS DIE LDYKPVVWFNLLVGLAYFAAVLSMIGDWLRVIS	300
ID	Q92OB6				Qy	256	AIVFVITLTGFDYVAGGS DIE LDYKPVVWFNLLVGLAYFAAVLSMIGDWLRVIS	315
AC	Q92OB6				Qy	301	KTTKEEVGEPRHAEEWVANVIAEKFETRRRLSVEIYDKEFQATSVKRLSAELGNHNQ	360
DT	01-DEC-2001	(TRMBLrel. 19, Created)			Qy	316	KTTKEEVGEPRHAEEWVANVIAEKFETRRRLSVEIYDKEFQATSVKRLSAELGNHNQ	375
DT	01-DEC-2001	(TRMBLrel. 19, Last sequence update)			Db	316	EUTPCRRTLSVNHLTSEREVLPPLKAKSIYINGLTHCAGDIAVENMK	411
DT	25-OCT-2004	(TRMBLrel. 28, Last annotation update)			Qy	361	EUTPCRRTLSVNHLTSEREVLPPLKAKSIYINGLTHCAGDIAVENMK	411
DB					Db	376	EUTPCRRTLSVNHLTSEREVLPPLKAKSIYINGLTHCAGDIAVENMK	426
DE					GN	Name=TREK-1;	Synonyme=KCNK2;	
DE					OS	Homo sapiens (Human);	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
GN	Name=Kcnk2;				OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OS	Rattus norvegicus (Rat);				OC			
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				OC			
OX					OC			
NCBI_TaxID	10116;				NCBI_TaxID	TaxID=9606;		
RN					RN	[1]		
RP					RP	SEQUENCE FROM N.A.		
RC	SEQUENCE FROM N.A.				RC	SEQUENCE FROM N.A.		
RC	TISSUE=Brain;				RC	SEQUENCE FROM N.A.		
RC	MEDLINE=21219399; PubMed=11319556;				RC	SEQUENCE FROM N.A.		
RA	Beckhauer D., Zilberman N., Goldstein S.A.;				RA	TISSUE=Brain;		
RA	"KCNK2, reversible conversion of a hippocampal potassium leak into a				RA	MEDLINE=20244931; PubMed=10784345;		
RT	voltage-dependent channel";				RA	RA		
RT	RT				RA	Meadows H.J., Benham C.D., Cairns W., Gloger I.S., Jennings C.,		
RT	RT				RA	RT		
RT	"KCNK2, reversible conversion of a hippocampal potassium leak into a				RA	"Cloning, localisation and functional expression of the human		
RT	voltage-dependent channel";				RT	orthologue of the TREK-1 potassium channel.";		
RT	RT				RT	RT		
RL	Nat. Neurosci. 4:486-491 (2001).				RL	PLoS Biol. 1(1):e1000006; doi:10.1371/journal.pbio.0010006		
RN					RN	[1]		
RP	SEQUENCE FROM N.A..				RP	SEQUENCE FROM N.A.		
RC	SEQUENCE FROM N.A..				RC	SEQUENCE FROM N.A.		
RC	SEQUENCE FROM N.A..				RC	SEQUENCE FROM N.A.		
RA	Gu W., Schlichterl G., Hirisch J.R., Engels H., Karschin C.,				RA	SEQUENCE FROM N.A.		
RA	RA				RA	SEQUENCE FROM N.A.		
RA	"Expression pattern and functional characteristics of two novel splice				RA	SEQUENCE FROM N.A.		
RT	variants of the two-pore-domain potassium channel TREK-2.";				RA	SEQUENCE FROM N.A.		
RT	RT				RA	SEQUENCE FROM N.A.		
RT	"Variants of the two-pore-domain potassium channel TREK-2.";				RA	SEQUENCE FROM N.A.		
RN	J. Physiol. 539:657-668 (2002).				RA	SEQUENCE FROM N.A.		
RP	SEQUENCE FROM N.A..				RA	SEQUENCE FROM N.A.		
RC	SEQUENCE FROM N.Wistar;				RA	SEQUENCE FROM N.A.		
RC	Li Z.B., Wang X.L.;				RA	SEQUENCE FROM N.A.		
RT	"Possible role of TREK-1 in temperature regulation.";				RA	SEQUENCE FROM N.A.		
RT	Submitted (JUL-2004) to the EMBL/Genbank/DBJ databases.				RA	SEQUENCE FROM N.A.		
CC	1- SIMILARITY: Belongs to the two pore domain potassium channel				RA	SEQUENCE FROM N.A.		
CC	(TC 1.A.1.8) family.				RA	SEQUENCE FROM N.A.		
DR	EMBL: AF25671; FAL01159.1; -.				RA	SEQUENCE FROM N.A.		
DR	EMBL: AF385402; FAL95708.1; -.				RA	SEQUENCE FROM N.A.		
DR	EMBL: AF695826; AAU06141.1; -.				RA	SEQUENCE FROM N.A.		
DR	GO; GO:00016020; C:membrane IEA.				RA	SEQUENCE FROM N.A.		
DR	GO; GO:0005216; F:ion channel activity; IEA.				RA	SEQUENCE FROM N.A.		
DR	GO; GO:0005267; P:potassium channel activity; IEA.				RA	SEQUENCE FROM N.A.		
DR	GO; GO:0006813; P:potassium ion transport; IEA.				RA	SEQUENCE FROM N.A.		
DR	PRINTS: PRO1333; 2PORECHANNEL.				RA	SEQUENCE FROM N.A.		
DR	PRINTS: PRO1499; TREKCHANNEL.				RA	SEQUENCE FROM N.A.		
RW	Ion transport; Ionic channel; Transmembrane; Transport.				RA	SEQUENCE FROM N.A.		
SQ	SEQUENCE 426 AA; 46912 MW; CACDA5BBE5FDBC CRC64;				RA	SEQUENCE FROM N.A.		
Qy	Query Match 98.6%; Score 2061; DB 2; Length 426;				RA	SEQUENCE FROM N.A.		
Qy	Best Local Similarity 98.3%; Pred. No. 4_1e-131;				RA	SEQUENCE FROM N.A.		
Qy	Matches 404; Conservative 3; Mismatches 4; Indels 0; Gaps 0;				RA	SEQUENCE FROM N.A.		
Db	1 MAAPDLIDPKSAQNSKPKRLSPSKPTASRVESDSPANVNMWKVTYSTIFLVVYLI				RA	SEQUENCE FROM N.A.		
Db	16 VAAPVKALEQOPQEISORTTIVIQKONFIQAHACVNSTELDELJQIVTAINAGIPLGNN				RA	SEQUENCE FROM N.A.		
Qy	61 GAAVPKALEQOPQEISORTTIVIQKONFIQAHACVNSTELDELJQIVTAINAGIPLGNN				RA	SEQUENCE FROM N.A.		

RA	Strausberg R.; Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.	RL	J. Biol. Chem. 277:49186-49199 (2002).
CC	-1- SIMILARITY: Belongs to the two pore domain potassium channel (TC 1.A.1.8) family.	CC	-1- SIMILARITY: Belongs to the two pore domain potassium channel (TC 1.A.1.8) family.
CC	EMBL; AF1068; AF89743_1; -.	CC	EMBL; AY148474; AAN37591_1; -.
DR	EMBL; EC069462; AAH69462_1; -.	DR	GO; GO:0016021; C:integral membrane; IEA.
DR	GO; GO:0016021; C:integral to membrane; IEA.	DR	GO; GO:0005216; F:ion channel activity; IEA.
DR	GO; GO:0005216; F:ion channel activity; IEA.	DR	GO; GO:0005267; F:potassium channel activity; IEA.
DR	GO; GO:0005267; F:potassium channel activity; IEA.	DR	GO; GO:0006813; P:potassium ion transport; IEA.
DR	GO; GO:0006813; P:ion transport; IEA.	DR	InterPro; IPR003280; K+channel_2pore.
DR	GO; GO:0006813; P:ion transport; IEA.	DR	InterPro; IPR001622; K+channel_pore.
DR	InterPro; IPR003280; K+channel_2pore.	DR	InterPro; IPR003976; Trek channel.
DR	InterPro; IPR001622; K+channel_pore.	DR	PRINTS; PR01333; 2PORECHANNEL.
DR	InterPro; IPR00376; Trek channel.	DR	PRINTS; PR01499; TREKCHANNEL.
DR	PRINTS; PR01333; 2PORECHANNEL.	KW	Ion transport; Ionic channel; Transmembrane; Transport.
RW	RW	SQ	SEQUENCE 411 AA; 45438 MW; A185EAC20A68CDC CRC64;
SEQUENCE 411 AA; 45438 MW; FDE40CAB21B42A1C CRC64;		Query Match	97.3%; Score 2034; DB 2; Length 411;
SEQUENCE 411 AA; 45438 MW; FDE40CAB21B42A1C CRC64;		Best Local Similarity	96.1%; Pred No. 2.6e-129;
SEQUENCE 411 AA; 45438 MW; FDE40CAB21B42A1C CRC64;		Matches	395; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
Query	1 MAAPDLIDPKSAAQNSKPRLSFSKPTVLASRVESDSDAINVMKWKTSTIFLVVVLYLII 60	Qy	1 MAAPDLIDPKSAAQNSKPRLSFSKPTVLASRVESDSDAINVMKWKTSTIFLVVVLYLII 60
Db	1 MAAPDLIDPKSAAQNSKPRLSFSKPTVLASRVESDSDAINVMKWKTSTIFLVVVLYLII 60	Db	1 MAAPDLIDPKSAAQNSKPRLSFSKPTVLASRVESDSDAINVMKWKTSTIFLVVVLYLII 60
Qy	61 GRAVKALEQPKIISORTTIVIQKQFIAHQCNSTDELIQIVAAAGIIPGNS 120	Qy	61 GAAVFKALEQPKIISORTTIVIQKQFIAHQCNSTDELIQIVAAAGIIPGNS 120
Db	61 GATVFKALEQPKIISORTTIVIQKQFIAHQCNSTDELIQIVAAAGIIPGNT 120	Db	61 GATVFKALEQPKIISORTTIVIQKQFISQHACVNSTDELIQIVAAAGIIPGNT 120
Qy	121 SNOVSHWDLGSSFFPAGTVTTGGNISPRTEGGKFCIYALGIPLGFLLAGVGDQ 180	Qy	121 SNOVSHWDLGSSFFPAGTVTTGGNISPRTEGGKFCIYALGIPLGFLLAGVGDQ 180
Db	121 SNOVSHWDLGSSFFPAGTVTTGGNISPRTEGGKFCIYALGIPLGFLLAGVGDQ 180	Db	121 SNOVSHWDLGSSFFPAGTVTTGGNISPRTEGGKFCIYALGIPLGFLLAGVGDQ 180
Qy	181 LGTFIGRGIAKVEDTFIKWNVSQTIKRILISTIIFLFGCVLFVALPAIFKHEGWSALD 240	Qy	181 LGTFIGRGIAKVEDTFIKWNVSQTIKRILISTIIFLFGCVLFVALPAIFKHEGWSALD 240
Db	181 LGTFIGRGIAKVEDTFIKWNVSQTIKRILISTIIFLFGCVLFVALPAIFKHEGWSALD 240	Db	181 LGTFIGRGIAKVEDTFIKWNVSQTIKRILISTIIFLFGCVLFVALPAIFKHEGWSALD 240
Qy	241 AIYFVITLTIGFDYAGGSDEIYDFYKPVWFLVGLAYFAAVLSMIGDWLRVIS 300	Qy	241 AIYFVITLTIGFDYAGGSDEIYDFYKPVWFLVGLAYFAAVLSMIGDWLRVIS 300
Db	241 AIYFVITLTIGFDYAGGSDEIYDFYKPVWFLVGLAYFAAVLSMIGDWLRVIS 300	Db	241 AIYFVITLTIGFDYAGGSDEIYDFYKPVWFLVGLAYFAAVLSMIGDWLRVIS 300
Qy	301 KTKKEEVBFRAAEWTANTVAEKFTRRLSVEYDKFQRATSVRKLSAELAGNHQ 360	Qy	301 KTKKEEVBFRAAEWTANTVAEKFTRRLSVEYDKFQRATSVRKLSAELAGNHQ 360
Db	301 KTKKEEVBFRAAEWTANTVAEKFTRRLSVEYDKFQRATSVRKLSAELAGNHQ 360	Db	301 KTKKEEVBFRAAEWTANTVAEKFTRRLSVEYDKFQRATSVRKLSAELAGNHQ 360
Qy	361 ELTPCRRTLSVNLHTSEREVLPPPLLKAHSIYLNGLTPHCAGEDIAVHENMK 411	Qy	361 ELTPCRRTLSVNLHTSEREVLPPPLLKAHSIYLNGLTPHCAGEDIAVHENMK 411
Db	361 ELTPCRRTLSVNLHTSERDVLPLKTESIYLNGLTPHCAGEIAVHENIK 411	Db	361 ELTPCRRTLSVNLHTSERDVLPLKTESIYLNGLTPHCAGEIAVHENIK 411
RESULT 5	SEQUENCE FROM N.A.	RESULT 6	SEQUENCE FROM N.A.
QHY88	PRELIMINARY; PRT; 411 AA.	CIW2_HUMAN	ID CIW2_HUMAN STANDARD; PRT; 426 AA.
ID QHY88;		AC 095059; QUNNE3;	AC 095059; QUNNE3;
AC QHY88;		DT 16-OCT-2001 (Rel. 40, Created)	DT 16-OCT-2001 (Rel. 40, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Created)		DT 16-OCT-2001 (Rel. 40, Last sequence update)	DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)		DT 05-JUL-2004 (Rel. 44, Last annotation update)	DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Potassium channel subfamily K member 2 (Outward rectifying potassium channel protein TREK-1) (TREK-1 K+ channel subunit) (Two-pore		DE Potassium channel subfamily K member 2 (Outward rectifying potassium channel protein TREK-1) (TREK-1 K+ channel subunit) (Two-pore	DE Potassium channel subfamily K member 2 (Outward rectifying potassium channel protein TREK-1) (TREK-1 K+ channel subunit) (Two-pore
GN Name=Kcnk2; Synonyms=TREK, TREK1;		GN Name=Kcnk2; Synonyms=TREK, TREK1;	GN Name=Kcnk2; Synonyms=TREK, TREK1;
OS Homo sapiens (Human);		OS Homo sapiens (Human);	OS Homo sapiens (Human);
OC Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;		OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.	OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
Bovinae; Bos.		NCBI_TaxID=9606;	NCBI_TaxID=9606;
OX [1]		RN [1]	RN [1]
RN SEQUENCE FROM N.A.		RP SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.
TISSUE_Adrenal cortex		RX MEDLINE=99254548; PubMed=10321245; DOI=10.1038/8084;	RX MEDLINE=99254548; PubMed=10321245; DOI=10.1038/8084;
RC Patel A.J., Honore B., Lesage F., Fink M., Romeo G., Jazdunski M.;		RA Patel A.J., Honore B., Lesage F., Fink M., Romeo G., Jazdunski M.;	RA Patel A.J., Honore B., Lesage F., Fink M., Romeo G., Jazdunski M.;
RM MEDLINE=22370953; PubMed=12368289; DOI=10.1074/jbc.M207233200;		RT "Inhalational anesthetics activate two-pore-domain background K+ channels." ; RT "An AChR- and ATP-regulated background K+ channel in adrenocortical	RT "Inhalational anesthetics activate two-pore-domain background K+ channels." ; RT "An AChR- and ATP-regulated background K+ channel in adrenocortical
RA Yearte J.J., Xu L., Danthi S., Enyeart J.A.;		RL RN [2]. Neurosci. 2:422-426 (1999). ; RL RN [2]. Neurosci. 2:422-426 (1999). ;	RL RN [2]. Neurosci. 2:422-426 (1999). ; RL RN [2]. Neurosci. 2:422-426 (1999). ;

RP	SEQUENCE FROM N.A.	Db	196 LGTIPGKGIAKVEDTDFIKWNVSQTKIRIISTIIFLFGCVLFVALPAVTKHIEGNSALD
RC	TISSUE=Brain; Price L.A.; Hellings S.E.; Hayashi J.H.; Pausch M.H.; Submitted (MAY-1997) to the EMBL/Genbank/DBJ databases.	Qy	241 AIFYFVVTLLTTGFGLYVAGGSDEIYLDFYKPVWFWFLVLGLAYFAAVLSMIGDWLRVVIS 300
RL	-!- FUNCTION: Outward rectifying potassium channel.	Db	256 AIFYFVVTLLTTGFGLYVAGGSDEIYLDFYKPVWFWFLVLGLAYFAAVLSMIGDWLRVVIS 315
CC	-!- SUBUNIT: Homodimer (Potential).	Qy	301 KCTKEEYGEFRAHAETANTAEKFTRRLSVEIYDKFQATSVKRKSAELAGHNQ 360
CC	-!- MISCELLANEOUS: Integral membrane protein (Potential).	Db	316 KCTKEEYGEFRAHAETANTAEKFTRRLSVEIYDKFQATSVKRKSAELAGHNQ 375
CC	-!- MISCELLANEOUS: Activated by volatile general anaesthetics such as chloroform, halothane and isoflurane.	Qy	361 ELTPCERLTLSVNHLTSEREVLPPLKRESIYINGLTPHCAGEDIAVIENMK 411
CC	-!- SIMILARITY: Belongs to the two pore domain potassium channel (TC 1.A.1.B) family.	Db	376 ELTPCERLTLSVNHLTSERDVLPLKTESIYINGLAPHCAGEDIAVIENIK 426
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).	RESUME 7	
CC	DR	EMBL; PF129399; AD47569.1; -.	Q60834 PRELIMINARY; PRT; 538 AA.
CC	DR	EMBL; AF004711; AD01203.1; -.	Q60834 PRELIMINARY; PRT; 538 AA.
CC	DR	GenBank; HGNC:6277; KCNK2.	AC 060834; PRELIMINARY; PRT; 538 AA.
CC	DR	MI:M; 63219; -.	DT 05-JUL-2004 (TrEMBLrel. 27, Created)
CC	DR	DR; GO:00016020; C:membrane; NAS.	DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
CC	DR	GO; GO:0015271; F:outward rectifier potassium channel activity; NAS.	DE Potassium channel TREK-2.
CC	DR	GO; GO:0006813; P:potassium ion transport; NAS.	GN Name=KCNK10;
CC	DR	InterPro; IPR003280; K+channel_2pore.	OS Oryctolagus cuniculus (Rabbit)
CC	DR	InterPro; IPR001622; K+channel_pore.	OC Buxarotid; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buttheria; Lagomorpha; Leporidae; Orcyctolagidae;
CC	DR	InterPro; IPR003916; Trek_channel.	OC NCBI_TaxID:9986;
CC	DR	PRINTS; PRO1333; 2PORECHANNEL.	RN [1] _SEQUENCE FROM N.A.
CC	DR	PRINTS; PRO1499; TREKCHANNEL.	RA Rae J.L.;
CC	KW	Glycoprotein; Ion transport; Ionic channel; Potassium; Potassium channel; Transmembrane; Transport; Voltage-gated channel.	RA Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC	KW	Potassium channel; Transmembrane; Transport; Voltage-gated channel.	-!- SIMILARITY: Belongs to the two pore domain potassium channel (TC 1.A.1.B) family.
FT	DOMAIN 1	61 Cytoplasmic (Potential).	CC EMBL; AY55324; AAS6599.1; -.
FT	TRANSMEM 62 82 Potential.	DR GO; GO:0016021; C:integral to membrane; IEA.	
FT	DOMAIN 144 170 Pore-forming 1 (Potential).	DR GO; GO:0005216; F:ion channel activity; IEA.	
FT	TRANSMEM 172 192 Potential.	DR GO; GO:0005267; F:potassium channel activity; IEA.	
FT	DOMAIN 193 223 Cycoplasmic (Potential).	DR GO; GO:0005811; P:ion transporth; IEA.	
FT	TRANSMEM 224 244 Potential.	DR GO; GO:0005813; P:potassium ion transport; IEA.	
FT	DOMAIN 253 283 Pore-forming 2 (Potential).	DR InterPro; IPR003280; K+channel_2pore.	
FT	TRANSMEM 288 308 Potential.	DR InterPro; IPR001622; K+channel_pore.	
FT	DOMAIN 309 426 Cytoplasmic (Potential).	DR InterPro; IPR003916; Trek_channel.	
FT	DOMAIN 378 426 Essential for chloroform and halothane sensitivity (By similarity).	DR PRINTS; PRO1333; 2PORECHANNEL.	
FT	DOMAIN 354 426 Required for basal channel activity (By similarity).	DR PRINTS; PRO1499; TREKCHANNEL.	
FT	CARBONYD 110 110 N-linked (GlcNAc. . .) (Potential).	RW Ion transport; Ionic channel; Transmembrane; Transport.	
FT	CARBONYD 134 134 N-linked (GlcNAc. . .) (Potential).	SQ SEQUENCE 538 AA; 59844 MW; 1F06GC8EA0DE8CB4D CRC64;	
FT	CONFICT 2 16 Missing (In Ref. 2).	Query Match Score 60.4%; Best Local Similarity 65.3%; Pred. No. 4.9e-77;	
FT	CONFICT 309 311 RLV > DWL (In Ref. 2).	Matches 247; Conservative 56; Mismatches 64; Indels 11; Gaps 5;	
FT	CONFICT 391 391 S > N (In Ref. 2).	Qy 2 AAPDLDDPKSAAQN - SKPRLSFSSKPTVLASRVESESDS--AINVMKKWKTYSTIFLFLVVV 56	
FT	CONFICT 411 411 A > T (In Ref. 2).	Db 23 APPVCOPKSATNGHPAPRLSISRSATVVA-RMEGTSGQGLQSVMKWTVAIFVWWVV 81	
SQ	SEQUENCE 426 AA; 4016 MW; 2ABA2336D4009F4E CRC64;	Qy 57 YLIIGAAVFKALEQPOBISQRTTIVOKQTFTAQHACVNSTELDELQOIVIAINAGIIP 116	
FT	DOMAIN 1 60 Score 2011; DB 1; Length 426;	Db 82 YLVTTGLVFLVRALEQPPESSQNTIALEKAEPFIRDHICVSPQELETIQHADANAGVSP 141	
FT	CONFICT 13; Mismatches 7; Indels 0; Gaps 0;	Qy 117 LGNSSNQYSHWDLGSSFFAGTVTTTGFGNNTSPRTGGKFCIYTALLGIPFLFGFLLAG 176	
FT	CONFICT 135	Db 142 IGNSSNNSSHWDLGSAFFAGTVTTTGFGNAPSTEGGKFCIYLAFGIPFLFGFLLAG 201	
FT	CONFICT 135	Qy 177 VGDQLGTLIFGKGIAKVEDTFLKWNVSQTKIRIISTIIFLFGCVLFVALPAVTKHIEG 236	
FT	CONFICT 135	Db 202 IGDQLGTFGKSIAVTEKVFRKCOVSKIRVSTIFLFLAGCIVFTIPAVTKYTBGW 261	
FT	CONFICT 135	Qy 237 SALDAYIPVVTLLTGFGLYVAGC-SDIEFLDFYKPVWFLVLGLAYFAAVLSMIGDW 295	
FT	CONFICT 135	Db 262 TALESIXFVVTLLTGYFDVAGNAGINREWYKPLWFWFLVLGLAYPAAVLSMIGDW 321	
FT	CONFICT 135	Qy 296 LRVISKTKKEEVGEFRAHAETWNTAETKTRRLSVEIYDFKQRATSV --- KRKL 351	
Qy	1 MAAPDLDPKSAQNSKPLSQQTIVOKQTFAQHACVNSTELDELQOIVIAINAGIIP 120		
Db	76 GATVKALEQPHETSQRTIVOKQTFSQHSCVNSTELDELQOIVIAINAGIIP 135		
Qy	121 SNQVSHWDLGSSFFAGTVTTTGFGNNTSPRTGGKFCIYTALLGIPFLFGFLLAG 180		
Db	136 SNQVSHWDLGSSFFAGTVTTTGFGNNTSPRTGGKFCIYTALLGIPFLFGFLLAG 195		
Qy	181 LGTIPGKGIAKVEDTFLKWNVSQTKIRIISTIIFLFGCVLFVALPAVTKHIEGNSALD 240		

Db	322	LRVLSKTCCTKEEIKAHAAEKANTTAEFTRRRLSVEHDKLQRAATRSMERRLG	381	RA	Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
Qy	352 AELAGHNINQELTPCRRTL	369	RA	Hori F., Imotani K., Ibihi Y., Itoh M., Kondo S., Kondo H., Kondo M., Koya S.,	
Db	382 LDQRAHSLDMLSPFRSV	399	RA	Kurinara C., Kawai J., Kojima Y., Matsuya T., Miyazaki A., Murata M., Nakamura M.,	
	RESULT 8		RA	Nishii K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,	
Q8BZB0	ID	PRELIMINARY;	PRT;	RA	Saito R., Saitoh H., Sakai C., Sakai K., Satazume N., Sano H.,
AC	Q8BZB0,			RA	Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
DT	01-MAR-2003	(TREMBLrel. 23, Created)		RA	Tanigawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
DT	01-OCT-2003	(TREMBLrel. 23, Last sequence update)		RA	Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
DE	Mus musculus	16 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone: 9630032C21 product: POTASSIUM CHANNEL SUBFAMILY K MEMBER 10 (OUTWARD RECTIFYING POTASSIUM CHANNEL PROTEIN TREK-2)		RA	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DE	(TREK-2 K+ CHANNEL SUBUNIT)	product: POTASSIUM CHANNEL PROTEIN TREK-2 (Fragment).		CC	-1 - SIMILARITY: Belongs to the two pore domain potassium channel (TC 1.A.1.8) Family.
OS	Mus musculus (Mouse).			CC	(TC 1.A.1.8) Family.
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Rodentia; Sciurognath; Muridae; Murinae; Mus.			DR	EMBL; AK036066; BAC9295.1; -.
OX	NCBI_TaxID=10090;			DR	GO; GO:0016021; C: integral to membrane; IEA.
RN	[1]			DR	GO; GO:0005216; F: ion channel activity; IEA.
RP	SEQUENCE FROM N_A.			DR	GO; GO:0005267; F: potassium channel activity; IEA.
RX	STRAIN=C57BL/6J; TISSUE=Cerebellum;			DR	GO; GO:0006811; P: ion transport; IEA.
RX	STRAIN=C57BL/6J; TISSUE=Cerebellum;			DR	GO; GO:0006813; P: potassium ion transport; IEA.
RX	MEDLINE=99291253; PubMed=10349336; DOI=10.1016/S0076-6879(99)03004-9;			DR	InterPro; IPR00380; K+channel_2pore.
RX	Carninci P., Hayashizaki Y.;			DR	InterPro; IPR001622; K+channel_pore.
RT	"High-efficiency full-length cDNA cloning.";			DR	InterPro; IPR003976; Trek channel.
RL	Meth. Enzymol. 30:19-44 (1999).			DR	PRINTS; PR01333; 2PORECHANNEL.
RN	[2]			DR	PRINTS; PR01499; TRIKCHANNEL.
RP	SEQUENCE FROM N_A.			DR	Ion transport; Ionic channel; Transmembrane; Transport.
RX	STRAIN=C57BL/6J; TISSUE=Cerebellum;			DR	KW
RX	STRAIN=C57BL/6J; TISSUE=Cerebellum;			PT	Non-TER
RX	STRAIN=C57BL/6J; TISSUE=Cerebellum;			SEQUENCE	453 AA; 49958 MW; FBCC3FF41E833E0 CRC64; /
Qy	YLIIGAAVAKFKALEQOPBISORTTIVIQKOTPIAQHACVNSTELLIQVIAAINAGIIP	116	Query Match	60.1%; Score 1256.5; DB 2; Length 453;	
Db	YLIIGAAVAKFKALEQOPBISORTTIVIQKOTPIAQHACVNSTELLIQVIAAINAGIIP	116	Best Local Similarity	65.3%; Pred. No. 9e-77; Matches 247; Conservative 55; Mismatches 65; Indels 11; Gaps 5;	
Qy	2 AAPDLIDPKSA--ADNSKPRLPSFSKPTPLASRVSDDS--AINTNWKWKTIVSTIFLYVVL	56	Matches	247; Conservatve 55; Mismatches 65; Indels 11; Gaps 5;	
Db	2 AAPDLIDPKSA--ADNSKPRLPSFSKPTPLASRVSDDS--AINTNWKWKTIVSTIFLYVVL	56	Qy	2 AAPDLIDPKSA--ADNSKPRLPSFSKPTPLASRVSDDS--AINTNWKWKTIVSTIFLYVVL	56
Qy	57 YLIIGAAVAKFKALEQOPBISORTTIVIQKOTPIAQHACVNSTELLIQVIAAINAGIIP	116	Db	2 AAPDLIDPKSA--ADNSKPRLPSFSKPTPLASRVSDDS--AINTNWKWKTIVSTIFLYVVL	56
Db	57 YLIIGAAVAKFKALEQOPBISORTTIVIQKOTPIAQHACVNSTELLIQVIAAINAGIIP	116	Qy	2 AAPDLIDPKSA--ADNSKPRLPSFSKPTPLASRVSDDS--AINTNWKWKTIVSTIFLYVVL	56
Qy	79 YLVGGIVFRALEQPPESSQSKNTIALEKFLRDHICVSPOLETLIQHALDADNAVGVP	138	Db	2 AAPDLIDPKSA--ADNSKPRLPSFSKPTPLASRVSDDS--AINTNWKWKTIVSTIFLYVVL	56
Qy	117 LGNSNQNQVSHWDGSAFFACTVTITFGNISPRTEGGKFLFCIIYALLGIPFLGPFLLAG	176	Qy	79 YLVGGIVFRALEQPPESSQSKNTIALEKFLRDHICVSPOLETLIQHALDADNAVGVP	138
Db	139 VGNSNQNQVSHWDGSAFFACTVTITFGNISPRTEGGKFLFCIIYALLGIPFLGPFLLAG	198	Db	79 YLVGGIVFRALEQPPESSQSKNTIALEKFLRDHICVSPOLETLIQHALDADNAVGVP	138
Qy	177 VGDQLQTIFGKGIAKYBDTFIKWNNSQTKRISTIIFLGCVLVALPAVIFKHIEGW	236	Qy	117 LGNSNQNQVSHWDGSAFFACTVTITFGNISPRTEGGKFLFCIIYALLGIPFLGPFLLAG	176
Db	199 IGDQLQTIFGKGIAKYBDTFIKWNNSQTKRISTIIFLGCVLVALPAVIFKHIEGW	258	Db	139 VGNSNQNQVSHWDGSAFFACTVTITFGNISPRTEGGKFLFCIIYALLGIPFLGPFLLAG	198
Qy	237 SALDAIYFWVITLTGTDYAGG-SDIEYLDFYKPVWVFMLWGLAYFAVLMSMIGDW	295	Qy	177 VGDQLQTIFGKGIAKYBDTFIKWNNSQTKRISTIIFLGCVLVALPAVIFKHIEGW	236
Db	259 TALESIYFVVVLTGFDVAGGNAGINYREWPKLWWFLWGLAYFAVLMSMIGDW	318	Db	199 IGDQLQTIFGKGIAKYBDTFIKWNNSQTKRISTIIFLGCVLVALPAVIFKHIEGW	258
RESULT 9	Q8BUW1	PRELIMINARY;	PRT;	Q8BUW1	PRELIMINARY;
Q8BUW1	ID	Q8BUW1		Q8BUW1	
AC	Q8BUW1;			AC	Q8BUW1;
DJ	01-MAR-2003 (TREMBLrel. 23, Created)			DJ	01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)			DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DT	Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length enriched library, clone:C230015H11 product:RICKS CHANNEL SUBFAMILY K MEMBER 10 (OUTWARD RECTIFYING POTASSIUM CHANNEL PROTEIN TREK-2)			DE	DE CHANNEL SUBUNIT homolog.
DE	DE Mus musculus (Mouse)			OS	OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
RA	RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,			OC	OC

OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	DR	PRINTS; PRO1333; 2POREKCHANNEL.
[1]	NCBI_TaxID=10090;	DR	PRINTS; PRO1499; TREKCHANNEL.
RN	SEQUENCE FROM N.A.	KW	Ion transport; Ionic channel; Transmembrane; Transport.
RP	STRAIN=C57BL/6J; TISSUE=Cerebellum;	SQ	SEQUENCE 535 AA; 59401 MW; 3E98E9F875C26BD CRC64;
RC	MEMLINE=9275253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;	Query Match	60.1%; Score 1256.5; DB 2; Length 535;
RX	RA Carninci P., Hayashizaki Y.;	Best Local Similarity	65.3%; Pred. No. 1..1e-76;
RX	RR "High-efficiency full-length cDNA cloning.";	Matches	247; Conservative 55; Mismatches 65; Indels 11; Gaps 5;
RL	Mech. Enzymol. 30:19-44 (1999).	QY	2 AAPDLDKPSA-AQNSPLRSFSKPKVLSRVEVS---ATNMWKWTKVSTFLVYVVL 56
RN	SEQUENCE FROM N.A.	Db	20 APPVCQPSATGHPVPLSTSATVVA-RMEGASQGLOTVMWKWTKVVAIFVVVVV 78
RP	STRAIN=C57BL/6J; TISSUE=Cerebellum;	QY	57 YLIGIAAVFKALEQPQETISQRTTIVQKQTFIAQHACVNSTELDELIQQIVAAINAGTIP 116
RC	MEMLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;	Db	79 YLVYGGLYVRADEQQPESQSQQNTIALAEKAERFDHICVSPOLETLIQLHALDDNAQVSP 138
RX	RA RIKEN FANTOM Consortium;	QY	117 LGNSSNQVSHWDLGSSPFAGTVTTGFGNISPRTCGGKFCIYALLGIPFLGFLLAG 176
RA	the RIKEN Genome Exploration Research Group Phase I & II Team;	Db	139 VGNSSNSSSHWDLGSAFFGQVTTGYNAPSTEGSKIFLYAIFGIPFLGFLLAG 198
RT	"Functional annotation of a full-length mouse cDNA collection.";	QY	177 VGBQLTIFGKGIAKEVTFIKVNSQSKIRISTTIFLFGCVLFALPAVFKHTEGW 236
RL	Nature 409: 685-690 (2001).	Db	199 IGDLQLTIFGKSTARVEKFRIKKQVSQSKIRVTSTIFLAGCIVFTIPAVTFKYEGW 258
RN	SEQUENCE FROM N.A.	QY	237 SALDAIYFVVFITLTIGFGDYVAGG-SDIEYLDFYKPVVWFVILGLAYFAAVLSMIGDW 295
RP	STRAIN=C57BL/6J; TISSUE=Cerebellum;	Db	259 TALESIYFVVFVLTIVFGDFVAGGNAGINTRYEWKPFLVWFVILGLAYFAAVLSMIGDW 318
RC	MEMLINE=20530913; PubMed=11076851; DOI=10.1101/gr.145100;	QY	296 LRVTSKETKEEVGEFHAAEWTANTAEFKETRRLSVETYDKFQRTATSV---KRKLS 351
RX	RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,	Db	319 LRVTSKETKEEVGEFHAAEWTANTAEFRTRRLSVETYDKFQRTATSV---KRKLS 378
RA	Konno H., Okazaki Y., Muranatsu M., Hayashizaki Y.;	QY	352 ABAGNNHQELTPCRRTL 369
RA	"Normalization and subbarcoding of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";	Db	379 LDORAHSLDMSEPKRSV 396
RT	RT prepare full-length cDNA libraries for rapid discovery of new genes.";	RESULT 1.0	
RL	Genome Res. 10:1617-1630 (2000).	C1WA_RAT	STANDARD; PRT; 538 AA.
RN	SEQUENCE FROM N.A.	ID	C1WA_RAT
RP	STRAIN=C57BL/6J; TISSUE=Cerebellum;	AC	Q2JIS4;
RX	MEMLINE=20530913; PubMed=11076851; DOI=10.1101/gr.145100;	DT	16-OCT-2001 (Rel. 40, Created)
RA	Shibata K., Itoh M., Aizawa K., NagaoKA S., Saigusa T., Katsunai T., Tashiro H., Itoh M.,	DT	16-OCT-2001 (Rel. 40, Last sequence update)
RA	Konno H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M.,	DT	05-JUL-2004 (Rel. 44, Last annotation update)
RA	Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Ikegami T., Kasaiwagi K., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kasaiwagi K.,	DE	Potassium channel subunit member 10 (outward rectifying potassium channel protein TREK-2) (TREK-2 K+ channel). Name=Ken10; Synonyms=Trek2;
RA	Fujiwake S., Inoue K., Togawa Y., Iizawa M., Ohara E., Watanuki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsushura S., Kawai J.,	GN	OS Ratnorvegicus (Rat);
RA	Okazaki Y., Muranatsu M., Inoue Y., Kira A., Hayashizaki Y.;	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RT	"RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";	OX	OC
RT	RT sequencing pipeline with 384 multicapillary sequencer.";	RN	SEQUENCE FROM N.A.
RL	Genome Res. 10:1577-1771 (2000).	[1]	SEQUENCE FROM N.A.
RN	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.
RP	STRAIN=C57BL/6J; TISSUE=Cerebellum;	RX	SEQUENCE FROM N.A.
RA	Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,	RA	SEQUENCE FROM N.A.
RA	Fukuda S., Furuno M., Hanabusa K., Sakai C., Sakai K., Hoshizume W.,	RA	SEQUENCE FROM N.A.
RA	Hayashida K., Hayatsu M., Hiramoto K., Hiraoka T., Hirozane T., Hori F., Imokuni K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,	RA	SEQUENCE FROM N.A.
RA	Katoh K., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,	RA	SEQUENCE FROM N.A.
RA	Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numasaki R., Ohno M., Ohbato N., Okazaki Y.,	RA	SEQUENCE FROM N.A.
RA	Sasaki R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shiogawa A., Shiraki T., Sogabe Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;	RA	SEQUENCE FROM N.A.
RA	Submitted (APR-2002) to the EMBL/Genbank/DDBJ databases.	RA	SEQUENCE FROM N.A.
CC	-1 SIMILARITY: Belongs to the two pore domain potassium channel (TC 1.A.1.B) family.	CC	-1 SUBCELLULAR LOCATION: Integral membrane protein (potassium channel).
CC	CC DR GO:0001601; C:internal to membrane; IBA.	CC	CC -1 TISSUE SPECIFICITY: Expressed mainly in the cerebellum, spleen, and testis.
CC	CC DR GO:0005216; F:potassium channel activity; IBA.	CC	CC -1 SIMILARITY: Belongs to the two pore domain potassium channel (TC 1.A.1.B) family.
CC	CC DR GO:0005267; F:potassium channel activity; IBA.	CC	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
CC	CC DR GO:0006813; P:potassium ion transport; IBA.	CC	CC
CC	CC DR InterPro; IPRO003280; K+channel_2pore.	CC	CC
CC	CC DR InterPro; IPRO01622; K+channel_pore.	CC	CC
CC	CC DR InterPro; IPRO03376; Trek_channel.	CC	CC

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CC	SEQUENCE FROM N.A. (ISOFORM A). MEDLINE=20435789; PubMed=1080510; DOI=10.1074/jbc.M002822200;
CC	RX Lesage F., Terrenoire C.; Romeo G., Lardunio M., RA "Human TREK2, a 2 P domain mechano-sensitive K <sup>+</sup> channel with multiple regulations by polyunsaturated fatty acids, lysophospholipids and Gs, G <sub>i</sub> , and G <sub>q</sub> protein-coupled receptors." RT J. Biol. Chem. 275:28398-28405 (2000).
CC	RL [2]
DR	RN SEQUENCE FROM N.A. (ISOFORMS B AND C). RP RX MEDLINE=21896087; PubMed=11897838;
DR	RA Gu W., Schlichter G., Hirsch J.R., Engels H., Karschin C., RA Karschin A., Perst C., Steinlein O.K., Daut J.; RA "Expression pattern and functional characteristics of two novel splice variants of the two-pore-domain potassium channel TREK-2."; RT J. Physiol. (Lond.) 539:657-668 (2002).
DR	RT RL - - FUNCTION: Outward rectifying potassium channel. Produces rapidly activating and non-inactivating outward rectifier K(+) currents. RT CC Activated by arachidonic acid and other naturally occurring unsaturated free fatty acids.
DR	RT CC - - SUBCELLULAR LOCATION: Integral membrane protein (Potential). RT CC - - ALTERNATIVE PRODUCTS: RT CC Event-Alternative splicing; Named isoforms=3; RT CC Name=A; Synonyms=tREK-2a; RT CC IsoId=P57789-1; Sequence=Displayed; RT CC Name=B; Synonyms=tREK-2b; RT CC IsoId=P57789-2; Sequence=VSP_006697; RT CC Name=C; Synonyms=tREK-2c; RT CC IsoId=P57789-3; Sequence=VSP_006698;
DR	CC - - TISSUE SPECIFICITY: Abundantly expressed in pancreas and kidney and to a lower level in brain, testis, colon, and small intestine. CC Isoform b is strongly expressed in kidney (primarily in the proximal tubule) and pancreas, whereas isoform c is abundantly expressed in brain.
DR	CC - - SIMILARITY: Belongs to the two pore domain potassium channel (TC 1.A.1.B) family.
DR	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).
DR	CC DR AF278890; AAC1519.1; -; DR AF335399; AAL95705.1; -; DR AF385400; AAL95706.1; -; DR Genew; HGNC: 6273; KCNK10. DR MIM: 605873; -; DR GO: GO:0005267; F: potassium channel activity; TAS. DR InterPro; IPR003280; K+channel_2pore. DR InterPro; IPR001622; K+channel_pore. DR InterPro; IPR003976; Trek channel. DR PRINTS; PR01333; 2POREKCHANNEL. DR PRINTS; PR01499; TREKCHANNEL. DR KW Alternative splicing; Glycoprotein; Ion transport; Ionic channel; KW Potassium; Potassium channel; Transmembrane; Transport; KW Voltage-gated channel.
DR	CC Cytoplasmic (Potential). CC Potential. CC Pore-forming 1 (Potential). CC Potential. CC Cytoplasmic (Potential). CC Potential. CC Pore-forming 2 (Potential). CC Potential. CC Cytoplasmic (Potential). CC N-linked (GlcNAc. . .) (Potential). CC N-linked (GlcNAc. . .) (Potential). CC MFFLYTDFFLSL -> MKGDRTEGCRSDS (in isoform B).
DR	CC DR RESULT 11 C1WA_HUMAN STANDARD; PRT; 538 AA. ID C1WA_HUMAN PRT; 538 AA. AC P57789; Q8TDK7; Q9HB59; DT 16-OCT-2001 (Re1 40, Created) DT 16-OCT-2001 (Re1 40, Last sequence update) DT 05-JUL-2004 (Re1 44, Last annotation update) DE Potassium channel subfamily K member 10 (Outward rectifying potassium channel protein TRK-2) (TREK-2 K <sup>+</sup> channel subunit). DE Name=KCNK10; Synonyms=TREK2; OS Homo sapiens (Human) OC Bacteria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarhinini; Hominidae; Homo. OC NCBI_TaxID=9606; RN

FT	VARSPLIC	1.	12	MFFLYTDFISL -> MKFPIETPRKQVNWDPK (in isoform C) 006698.	RA	Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human RT and mouse cDNA sequences." / Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
FT	CONFLICT	529	529	E -> G (in Ref. 2).	RT	
FT	SEQUENCE	538 AA;	59764 MW;	8EA615B08D147FBC CRC64;	RL	
SQ					RN	[2]
					RP	SEQUENCE FROM N.A.
					RC	TISSUE-Pooled tissue;
					RA	Director MGC Project;
					RL	Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
					DR	EMBL; BC075022; AAH75022.1;
					DR	GO; GO-0016020; C:membrane; IEA.
					DR	GO; GO-0005116; F:ion channel activity; IEA.
					DR	GO; GO-0005267; F:potassium channel activity; IEA.
					DR	GO; GO-0008813; P:potassium ion transport; IEA.
					DR	IPR003280; K+channel 2 pore.
					DR	IPR001622; K+channel pore.
					DR	IPR011255; NLR SiRaiPha_1/3.
					DR	IPR003976; Trek channel.
					DR	PRINTS; PRO1333; 2POREBKCHANNEL.
					DR	PRINTS; PR01499; TREKCHANNEL.
					KW	Ionic channel.
					SQ	SEQUENCE 543 AA; 60110 MW; 17DB1AFAPAB07C46 CRC64;
					Query	Match Score 59.9%; Score 1251.5%; DB 2; Length 543;
					Best Local Similarity	64.3%; Pred. No. 2.3e-76;
					Matches	247; Conservative 54%; Mismatches 66%; Indels 17; Gaps 5;
					Qy	2 AAPDLDPDKSA-----AQNSKPLRSSSKPTVLASREVSDS--AINYMKWKVTSTI 50
					Db	17 AAAPVCQPKSATNGQPPAPTPPRLSSRATVVA-RMEGTSQGGQTQVWKWKTVAI 75
					Qy	51 FLVVLVLTIGAAVKALEQPOEISORTTIVIKQTFAHQACVNSTNLQITVAI 110
					Db	76 FVVVVVILVTTGGLYFRAEQPFESSQNTIALEKAERFDAYCVSPQLETLIQHALDAD 135
					Qy	111 NAGTIPQNSNQVSHWLQDGSSPFAGTVTTTGFGNISPRTEGGKTCITYALLGIPLF 170
					Db	136 NAGVSPGISSNSNNSSHWLQDGSAFFGKTAEVGTVTTTGFGNAPSTGGKFCILAFGIPLF 195
					Qy	171 GFLLAGVGQDOLGTIFGKGIAKVEDFTFKRNVSOTKIRVISTILFILPCVLFALPAVIF 230
					Db	196 GFLLAGVGQDOLGTIFGKSTARVEKVFRKQSVQTAKRVSQTKIRVISTILFILLAGCIVFTIPAVIF 255
					Qy	231 KHTEGWSALDATIVFVTTTIGDGYAGG-SDIEYDQVWTFILVGLAYFAAVL 289
					Db	256 KYEGTWALESIYFVWVLTGDFAGGNAGINFEKFWYKPLWVFILVGLAYFAAVL 315
					Qy	290 SMIGDWLRVISKTKTKEEYGEFRAAENTANTYAEKFETRRLSVEIYDFKQFATSV-- 346
					Db	316 SMIGDWLRVISKTKTKEEYGEFRAAENKANTYAEFETRRLSVEITHDKLORAATIRSM 375
					Qy	347 -KRLKLSAELAGNNQELTPCRTL 369
					Db	376 ERRRLGQIQLQRASHLDMLSPEKRSV 399
					RESULT 12	
					QEB014	SEQUENCE FROM N.A.
					ID QEB014;	SEQUENCE-Pooled tissue;
					AC QEB014;	MEELINB-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
					DT 25-OCT-2004 (TREMBLrel. 28, Created)	
					DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)	
					DE Potassium channel, subfamily K, member 10, isoform 3.	
					OS Name=KCNK10;	
					Homosapiens (Human).	
					Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;	
					Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
					NCBI_TAXID=9606;	
					RN [1]	
					RP	SEQUENCE FROM N.A.
					RX MEELINB-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;	
					RA Klausen R.L., Derge J.G., Grouse L.H., Feingold E.A., Shemer R.N.K., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Blat N.K., Diatchenko L., Marusina K., Farmer A.A., Bonaldo M.F., Casavant T.B., Scheetz T.B., Brownstein M.J., Usdin T.B., Carrinci P., Orange C., Raha S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mullany S.J., Bozak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Villalona D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., RA Krzywinski M.I., Skalska U., Smailus D.E., Scherich A., Schein J.E., RA	RESULT 13
					RA	PRELIMINARY; PRT; 546 AA.
					RA	Q68EY1 ID Q68EY1 PRELIMINARY; PRT; 546 AA.
					RA	Q68EY1 AC Q68EY1 PRELIMINARY; PRT; 546 AA.
					RA	Q68EY1 DT 25-OCT-2004 (TREMBLrel. 28, Created)
					RA	Q68EY1 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
					RA	Q68EY1 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
					RA	Q68EY1 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
					RA	Q68EY1 DE LOC446788 Protein (Fragment).
					RA	Q68EY1 GN Name=LOC446788; Name=Xenopus laevis (African clawed frog).
					RA	Q68EY1 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrates; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Xenopoda; Xenopus.
					RA	Q68EY1 OC NCBI_TAXID=3355;
					RA	Q68EY1 RN SEQUENCE FROM N.A.

TISSUE=Eye;	Klein S.I., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;	
Richardson P.;	
"Genetic and genomic tools for Xenopus research: The NIH Xenopus initiative.";	
Dev. Dyn. 225:384-391 (2002).	
[2]	
SEQUENCE FROM N.A.	
SEQUENCE=Eye;	
PubMed=12477932; DOI=10.1073/pnas.242603899;	
Peingold R.L., Grouse L.H., Derge J.G., Schuler G.D.,	
Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Bhat N.K.,	
Aleschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Wang J.J., Hsieh F.,	
Hains R.F., Jordan H., Moore T., Max S.I., Rubin G.M., Hong L.,	
Diatchenko L., Marsina K., Farmer A.A., Casavant T.L., Scheetz T.E.,	
Scapleton M., Soares M.B., Donald M.F., Carninci P., Prange C.,	
Brownstein M.J., Osdin T.B., Toshiyuki S., Loguello N.A., Peters G.J., Abramson R.D., Mullay S.J.,	
Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	
Boesak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gay L.J., Hulyk S.W.,	
Richards S., Worcester K.C., Hale S., Garcia A.M., Villalobos D.K., Murry D.M., Soderberg E.J., Lu X., Gibbs R.A.,	
Fainey J., Heitton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,	
Whiting M., Madan J., Young A.C., Shevchenko Y., Bouffard G.G.,	
Blaikley R.W., Touchman J.W., Green E.D., Dickson M.C.,	
Rodriguez A.C., Grimmwood J., Schmutz J., Myers R.M., Butterfield Y.S.,	
Krzywinski M.I., Smialius D.E., Schein J.E., Jones S.J., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human	
and mouse cDNA sequences.";	
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	
[3]	
SEQUENCE FROM N.A.	
SEQUENCE=Eye;	
Klein S., Gerhard D.S.;	
Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.	
EMBL: BC080069; AA080069.1; -	
InterPro: IPR003280; K+channel_2 pore.	
InterPro: IPR001622; K+channel_1 pore.	
PRINTS: IPR003976; Trek channel.	
PRINTS: PRO1333; 2POREKCHANNEL.	
NON TER 546 546 AA; 60977 MW; AP6C7FB24AD3AA06 CRC64;	
SEQUENCE	
Query Match 58 5% ; Score 1223 5; DB 2; Length 546;	
Best Local Similarity 60.6%; Pred. No. 1.8e-74;	
Matches 241; Conservative 62; Mismatches 70; Indels 25; Gaps	
18 PRLLSSKKPVTLASRVESDAI-NYNNWKWTVSTIFLVVVLIGAVPKALEQPOBISO 7	
52 PRMSVCRSRSTIVSTMNTSSCLHSYMKWKTVAIFVVVVVLYVLTGSLVFRALEQPEFSSQ 1	
77 RTTIVTQKOFFIAQFACVNSTELDENIQQIVAAINGIITIPGNNSNQVSHDGLSAFFFA 1	
112 KSTTAQEKSDFLHNHPCVTQOELDAJKAIDADNGVNPNFTNYNSSSSHDGLSAFFFA 1	
137 GTVITITGFGNISPRTEGGKIFCITYALLGIPLFGLLAGDQLTIGKGIAKYBDF 1	
172 GTVITITGFGNIAPISTEGGKIFCILYAIFGPFLAGDQLTIGKSIARVEKF 2	
197 IKWNYSQTQKIRIISTIIFLGCVLEVALPAVTFKIEGWSALDAYFVWLTITGFD 2	
232 LKQVQSQTQKIRIISTIIFLVAGCLVFTVTPAVIFQIEGWTELESIVVVVLTIGFD 2	
257 YVAGG-SDIEYLDEFKPVWVFWLIVGLAYFAAVLSMGTWDWRVISKTTKEVGEFAHAA 3	
292 FVAGGNTDISREWTKPLWVFWLIVGLAYFAAVLSMGTWDWRVISKTTKEVGEFAHAA 3	
316 EWANTVTAEEKETTRRLSVEIYDKFORATSV---KRKLSSAELAGNHNQELTPCRRTL-- 3	
352 EWKANTVTAEEKETTRRLSVEIYDKFORATSV---KRKLSSAELAGNHNQELTPCRRTL-- 3	

Qy	370	----- SVNHLTSEREVLPPLKAESIYLYG 394
Db	412	ELEAGGRFKASSQOSINNRPNNLR --- LKEAEQFTLHG 445
RESULT 14		
CIW4_HUMAN	CTW4_HUMAN	STANDARD; PRT; 393 AA.
ID	Q96794;	
AC	Q96794;	
DT	16-OCT-2001 (Rel. 40, Created)	
DT	16-OCT-2001 (Rel. 40, Last sequence update)	
DT	05-JUL-2004 (Rel. 44, Last annotation update)	
DB	Potassium channel subfamily K member 4 (TWIK-related stimulated potassium channel protein) (TRAAK) (Two)	
DE	KM4_1).	
DE	Name=KCNK4; Synonyms=TRAAK;	
GN	OS Homo sapiens (Human).	
OC	Ukaryota; Metazoa; Chordata; Vertebrata;	
OC	Mammalia; Butheria; Primates; Catarrhini; Hominoidea	
OX	NCBI_TaxID=9606;	
RN	[1]	
RP	SEQUENCE FROM N.A. (ISOFORM 1).	
RC	TISSUE=Brain;	
RX	PMID:1012359; DOI=10.1016/S0169-328X(00)00183-2;	
RA	Chapman C.G., Meadows H.J., Godden R.J., Campbell D.	
RA	Kelsell R.E., Murdock P.R., Randall A.D., Rennie G.	
RT	"Cloning, localisation and functional expression of cerebellum specific, two pore domain potassium chan-	
RT	Brain Res. Mol. Brain Res. 82:74-83 (2000).	
RL	[2]	
RN	SEQUENCE FROM N.A. (ISOFORM 1).	
RC	TISSUE=Frontal cortex;	
RA	Gray A.T.;	
RT	"Assignment of KCNK4 encoding the human potassium c-	
RT	romosome 11.";	
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ database.	
RN	[3]	
RP	SEQUENCE FROM N.A. (ISOFORM 1).	
RX	MedlineID=2031699; PubMed=10167409; DOI=10.1016/S001	
RA	Lesage F., Maincret F., Larduski M.;	
RT	"Cloning and expression of human TRAAK, a polyunsat-	
RT	urated and mechano-sensitive K(+) channel 1."	
RL	FEBS Lett. 471:137-140 (2000).	
RN	[4]	
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).	
RX	MedlineID=22178385; PubMed=12191490; DOI=10.1016/S016	
RA	Ozaita A., Vega-Saenz de Miera E.;	
RT	"Cloning of two transcripts, HK4.1a and HK4.1b, f-	
RT	pore K <sup>+</sup> channel gene KCNK4. Chromosomal localization,	
RT	distribution and functional expression."	
RL	Brain Res. Mol. Brain Res. 102:18-27 (2002).	
RN	[5]	
RP	SPlice ISOFORM(S) THAT ARE POTENTIAL NMN TARGET(S).	
RX	PubMed=1475258; DOI=10.1186/gb-2004-5-2-r8;	
RA	Hillman R.T., Green R.E., Brenner S.E.;	
RT	"An unappreciated role for RNA surveillance;"	
RL	Genome Biol. 5:RESEARCH008.1-RESEARCH008.16 (2004).	
CC	-1- FUNCTION: Voltage insensitive, instantaneous, o-	
CC	potassium channel. Outward rectification is rev-	
CC	external K(+) concentrations (By similarity).	
CC	-1- SUBUNIT: Homodimer (Potential).	
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.	
CC	-1- ALTERNATIVE PRODUCTS:	
CC	Event=Alternative splicing; Named isoforms=2;	
CC	Name=1; Synonyms=K4.1a;	
CC	Isoid=Q9NYC8-1; Sequence=Displayed;	
CC	Name=2; Synonyms=KM4_1b;	
CC	Isoid=Q9NYC8-1; Sequence=VSP_005689;	
CC	Note=May be produced at very low levels due to codon in the mRNA, leading to nonsense-mediated	
CC	-1- SIMILARITY: Belongs to the two pore domain pota-	
CC	(TC 1.A.1.8) family.	

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CC	DE Potassium channel subfamily K member 4 (TWIK-related arachidonic acid-stimulated potassium channel protein) (TRAAK).
CC	DS Name=Kcnk4; Synonyms=TRAAK;
CC	GN Mus musculus (Mouse).
CC	OS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butchero; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC	OC NCBI_TaxId=10909;
CC	OX RN [1]
DR	SEQUENCE FROM N.A.
DR	TPISUE:Brain; MEDLINE=98292450; PubMed=9628867; DOI=10.1093/embj/17.12.3297;
DR	Rink M., Lesage F., Duprat F., Heurteaux C., Reyes R., Fosset M., Lazdunski M.
DR	RT "A neuronal two P domain K <sup>+</sup> channel stimulated by arachidonic acid and polyunsaturated fatty acids.";
DR	RT RN [1]
DR	EMBL: AP248242; AAC31731.1; ALT_INIT.
DR	EMBL: AF640622; AF274042; AF259500; AF49369.1; -.
DR	EMBL: AF259501; AF49390.1; -.
DR	GeneID: HGNC:2279; KCNK4.
DR	MIM: 605720; -.
DR	GO: GO:0005267; P:potassium channel activity; TAS.
DR	GO: GO:0006813; P:potassium ion transport; TAS.
DR	InterPro: IPR003880; K+channel_2pore.
DR	InterPro: IPR01622; K+channel_pore.
DR	InterPro: IPR008074; TRAAK_channel.
DR	PRINTS: PRO1333; 2POREKCHANNEL.
DR	PRINTS: PRO1691; TRAAKCHANNEL.
KW	Alternative splicing; Glycoprotein; Ion transport; Ionic channel;
KW	Potassium; Potassium channel; Transmembrane; Transport;
KW	Voltage-gated Channel.
FT	TRANSMEM 1 3
FT	TRANSMEM 4 24
FT	TRANSMEM 89 113
FT	TRANSMEM 118 138
FT	TRANSMEM 139 171
FT	TRANSMEM 172 192
FT	TRANSMEM 197 221
FT	TRANSMEM 234 254
FT	TRANSMEM 255 393
FT	CARBOHYD 78 78
FT	CARBOHYD 82 82
FT	VARSPLIC 1 1
FT	CONFFLICT 328 328
FT	SEQUENCE 393 AA; 42704 MW; 7F18E3A0A9AD57D CRC64;
Qy	Query Match Score 797; DB 1; Length 393;
Db	Best Local Similarity 51.1%; Prod. No. 8.1e-46; Matches 145; Conservative 60; Mismatches 77; Indels 2; Gaps 1;
Qy	42 MKWKTIVSTIFLVVLYLIGAFKALQPOETQSRTIVIQKOTFLQHACYNSTLDE 101
Db	1 MRSTLLALLALVLYLGSVALRQLPHEOAQRLEGEYKEFLAHPCVSQDEGL 60
Qy	102 LIQIVVAIAINAGI1PLGNSSNQVSH--WDLGSSFFFAFGSTVITIGEHNMSPTTEGGKFC 159
Db	61 LIKEVADLGGADEPTNTSNSHSWAIDLGSAFFSTIITIGVNAVALTDAGRIFC 120
Qy	150 IIALLGGPLFLGFLLAGQDQLGTIGFGKIAKVEDFTFKWNVQSTKRIISTIPIFLGC 219
Db	121 IFLALVG1PLFGLLAGDRLGSSLRIGIGHAEFLKWHVPPLEVLSAMLFULLGC 180
Qy	220 VFLGLAYPAVIFRHEWYFWVLTGAGSDIEYLDFYKPVWWFIL 279
Db	181 LLFFLTFPVFCMEDWSKLEAVYFVVLTVGFDTAGDRQDSPAYQLVWFML 240
Qy	280 VGLAYFAVISMIGDWLKVSKTKPEKEVGEFRHAASENTANTYA 323
Db	241 LGLAYFASVLTGIVNWLRRTRAEVNGGLTAQAASTGTGTVTA 284
RESULT 15	
ID_CTW4_MOUSE	STANDARD; PRT; 398 AA.
AC 088454;	
DT 16-OCT-2001 (Rel. 40, Created)	
DT 16-OCT-2001 (Rel. 40, Last sequence update)	
DT 05-JUL-2004 (Rel. 44, Last annotation update)	

Search completed: July 13, 2005, 08:44:31  
Job time : 95.9622 secs



A; Molecule type: DNA  
 A; Residues: 1-310 <KIM>  
 A; Cross-references: GB:AU119522  
 C; Comment: This protein, a new member of the tandem-pore K<sup>+</sup> channel family with four transmembrane segments, but does not produce a functional plasma membrane K<sup>+</sup> current by itself  
 C; Genetics:  
 A; Gene: task-5  
 A; Map position: 20g12  
 C; Keywords: transmembrane protein  
 F; 1-7-10/Domain: transmembrane segment #status predicted <TMS1>  
 F; 107-128/Domain: transmembrane segment #status predicted <TMS2>  
 F; 129-155/Region: hydrophobic cytoplasmic linker  
 F; 156-180/Domain: transmembrane segment #status predicted <TMS3>  
 F; 220-240/Domain: transmembrane segment #status predicted <TMS4>

Query Match 16.8%; Score 351.5; DB 2; Length 330;  
 Best Local Similarity 35.0%; Pred. No. 6.6e-21;  
 Matches 91; Conservative 44; Mismatches 94; Indels 31; Gaps 8;

Db 111 LVLCTLCLVVAEEVALEESBAE-SGRQLIVQRGALRKFGFSAEDRELRLAQAA 69

Qy 110 --INAGIPLGNSSNQVSHWDLGSSPFFACTWTTIGFGENISPRTEGGKICITYALLGI 167

Db 70 EPHRAG-----RQWKPGPSFYFAITYVTTIGYGHAPGTDGSKVCFMAYLLGI 118

Qy 168 PLEGFLLAGVGPDGLGTIPKGKIAKVEDTF-IKWNTSQTQKRILISTIFLPGCVLFVALP 226

Db 119 PLTLVTQFSQSLGERLNATVRILLIAAKCCLGLRWTCVSTE---NLVAGULLACATTALG 174

Qy 227 AVTKHIEGWSALDAITYFVVITLTGFDYVAGGSDEIYLDFYKEVWWF--WLVGLA 283

Db 175 AVAFSHEGWTFHAYYCFTLTTIGFDVFVALQSG-EALQRKLPVYAFSPFLYILLGLT 233

Qy 284 YFAAVLSMI-----GDW 295

Db 234 VIGAFNLNVLRFLVASADW 253

**RESULT 3**  
 T43509 probable potassium channel chain n2P38 - Caenorhabditis elegans  
 C; Species: Caenorhabditis elegans  
 C; Accession: T43509  
 R; Wang, Z. W.; Salkoff, L.  
 Submitted to the EMBL Data Library, August 1998  
 A; Description: Potassium channels in C. elegans.  
 A; Reference number: Z2450  
 A; Accession: T43509  
 A; Status: Preliminary; translated from GB/EMBL/DDJB  
 A; Residues: 1-329 <WAN>  
 A; Cross-references: UNIPROT:O17185; EMBL:AF083652; PIDN: AAC32863.1

Query Match 16.4%; Score 343; DB 2; Length 329;  
 Best Local Similarity 34.1%; Pred. No. 3.2e-20;  
 Matches 94; Conservative 53; Mismatches 95; Indels 34; Gaps 11;

Db 42 MKWKTVDSTIELVY-VLYLIIGAAVEKALEQPEQEIISORTTIVIQKQTFAQHACVNSTEL 99

Db 1 MRQNIRTLSTLVIYCTYLGVAAVEPALETEENIQLQRKLYQVRVREKLTKTYNNMENA-DV 59

Qy 100 DELIQQTVAII--NAGIIPLGNSSNQVSHWDLGSSPFFACTWTTIGFGENISPRTEGGKI 157

Db 60 EILEATIVKTSVPHKAGY-----QWKESGAFYPATVITIGYGHSTPMDAGKV 108

Qy 158 FCITYALIGIPIFGFLLAGVGPDGLGTIPKGKIAKVEDTFIKWNVSQKIRISTIIFLIF 217

Db 109 FCMLYALZGIPCLIMQFSIGERMNTPAKLL----RFIRRAAGKOPIVTSSDLMIFCT 163

Qy 218 GC-VLFVY-FFPSLV---FILGLTVISAAMNLL--VLRFLTMNTEDE 260

Db 164 GWGGGLIFGGAFMFSSSYENNTYFDAAVYCFVTLTIGFGBDYVALQKRGSLQTOPPVY-FF 222

Qy 271 KPVVVFVILVGLAYPAVLSMIGDWLRVISKKTKE 306

Db 223 SLV--FILFGLTVISAAMNLL--VLRFLTMNTEDE 253

**RESULT 4**  
 T32347 outward rectifier potassium channel homolog twk-23 - Caenorhabditis elegans  
 C; Species: Caenorhabditis elegans  
 C; Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
 R; Murray, J.; Wohlbachmann, P.; O'Neal, D.  
 A; Description: submitted to the EMBL Data Library, September 1997  
 A; Reference number: Z221153  
 A; Accession: T32347  
 A; Status: preliminary; translated from GB/EMBL/DDJB  
 A; Molecular type: DNA  
 A; Residues: 1-336 <MUR>  
 A; Cross-references: UNIPROT:O17185; EMBL:AF025454; PIDN: AAC71151.1; GSPDB: GN00020; CESP:  
 C; Genetics:  
 A; Gene: twk-23; CESP:F34D6.3  
 A; Map position: 2  
 A; Introns: 44/3; 102/1; 136/1; 180/1; 207/1; 265/2; 296/3

Query Match 15.8%; Score 329.5; DB 2; Length 336;  
 Best Local Similarity 33.2%; Pred. No. 4.1e-19;  
 Matches 94; Conservative 53; Mismatches 95; Indels 41; Gaps 12;

Db 42 MKWKTVDSTIELVY-VLYLIIGAAVEKALEQPEQEIISORTTIVIQKQTFAQHACVNSTEL 99

Db 1 MRQNIRTLSTLVIYCTYLGVAAVEPALETEENIQLQRKLYQVRVREKLTKTYNNMENA-DV 59

Qy 93 CVNSPDELIDLQQIYAAI--NAGIIPLGNSSNQVSHWDLGSSPFFACTWTTIGFGENISPRTEGGKI 150

Db 61 MSNA-DYEILEATIVKTSVPHKAGY-----QWKESGAFYPATVITIGYGHSTPMDAGKV 92

Db 151 RTEGGKXIFCITYALIGIPIFGFLLAGVGPDGLGTIPKGKIAKVEDTFIKWNVSQTKIRIIS 210

Db 109 MTDA4VKFCMLYALGAPIGLIMFQSIGERMNTPAKLL----RFIRRAAGKOPIVTSS 163

Qy 211 TIIFLIFGCV-LVLFVLPAVFKHTGWSALDAITYVPTLTTIGFDDYVA--GCS---D 263

Db 164 DLIFITCGWGLLFGMFSYNTWYDPAVYCFVTLTIGFDDYVALQKRGSLQTO 223

Qy 264 IEYLDIYKPVYVFWFLVGLAYPAVLSMIGDWLRVISKKTKE 306

Db 224 PEYV-FFPSLV---FILGLTVISAAMNLL--VLRFLTMNTEDE 260

**RESULT 5**  
 T13807 potassium channel protein - fruit fly (*Drosophila melanogaster*)  
 C; Species: *Drosophila melanogaster*  
 C; Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 09-Jul-2004  
 C; Accession: T13807  
 R; Goldstein, S.A.; Price, L.A.; Rosenthal, D.N.; Pausch, M.H.  
 Proc. Natl. Acad. Sci. U.S.A. 93, 13256-13261, 1996  
 A; Title: ORK1, a potassium-selective leak channel with two pore domains cloned from *Drosophila*  
 A; Reference number: Z17770; PMID: 97075152  
 A; Status: preliminary; translated from GB/EMBL/DDJB  
 A; Molecular type: mRNA  
 A; Residues: 1-100 <GOL>  
 C; Genetics:  
 A; Gene: ORK1  
 A; Cross-references: UNIPROT:Q94526; EMBL:U55321; PIDN: G3808067; PIDN: AAC692  
 A; Map position: 1

Query Match	15.6*	Score 325; DB 2; Length 1001;	Qy	278 ILVGLAYP-----AAVLSMIGDWLRLVISKKTKTKEEYGEFRAAETANTVTAEFKETTR 330
Best Local Similarity	28.8*	Pred. No. 3.5e-18;	Db	302 LTGACPFYCLSNVNSSTIVVROLLNNM---IKCMDVKV7-EDRSFLC-----FCKKRR 348
Matches	90; Conservative	62; Mismatches 125; Indels 36; Gaps 10;	Qy	331 RLSV 334
Db	9 LLIYFISYLMFGAIYIYIEHGBEKISRAEQKAQIANEYELLELGDKNTTQDELLQR 68		Db	349 YMGL 352
Qy	106 IVAAINACITIPLGNSNSQVSHDGLGSSPTTDPYTYHAFPFIAFTVCSITPRTEGGKIFCITYALL 165	RESULT 7	Qy	278 ILVGLAYP-----AAVLSMIGDWLRLVISKKTKTKEEYGEFRAAETANTVTAEFKETTR 330
Db	69 ISDYCDKETVLTLPPTDPPYTYHAFPFIAFTVCSITPRTEGGKIFCITYALL 128	T19860	Db	302 LTGACPFYCLSNVNSSTIVVROLLNNM---IKCMDVKV7-EDRSFLC-----FCKKRR 348
Qy	166 GIPLEGPLLAGVGDLQGTFKGKIAKVEDTFIKWNV-----QTKIRIISNIIFLFG 218	hypothetical protein C40C9.1 - Caenorhabditis elegans	C;Species: Caenorhabditis elegans	
Db	129 GIPVNGTLFLAG----LGFGTFFEAITYRKYCKKMKSTDMDHYTPPQLGLITTVIALPG 184	C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000	C;Accession: T19860	
Qy	219 CVLFVALPAVIFKHIEGMSALDAIYFVVTUTLTFGDDYVA-----GGSDIEYLD 268	R;Embry: C	R;Embry: C	
Db	185 IALFLPLSWFVTFYFENWPYSISLYSVTITIGSDYVPTFGANOPKEPSGWFWVYQI 244	Submitted to the EMBL Data Library, March 1996	Submitted to the EMBL Data Library, March 1996	
Qy	269 FYKPVVWFWIYLGLAYPAVLMSIGDWLRVISRK---TKEEVGEFFAETANTVTAE 324	A;Reference number: Z19188	A;Reference number: Z19188	
Db	245 FV--IWWH--IFSLGLVNMIMTFITRGL--SKRLAYLEQQQLSSNLKATQNRIWSGVTKD 298	A;Cross-references: EMBL:Z70266; PIDN:CAA94204.1; GSPDB:GN00028; CESP:C40C9.1	A;Cross-references: EMBL:Z70266; PIDN:CAA94204.1; GSPDB:GN00028; CESP:C40C9.1	
Qy	325 FKETRRRLSVEIY 337	A;Experimental source: clone C40C9	A;Experimental source: clone C40C9	
Db	299 VGYLRRMLN-ELY 310	C;Genetics:	C;Genetics:	
Qy	13.8*	A;Gene: CESP:C40C9.1	A;Gene: CESP:C40C9.1	
Db	109 VGYLRRMLN-ELY 310	A;Map Position: X	A;Map Position: X	
Qy	13.7*	A;Introns: 34/1; 6/0/2; 98/1; 145/3; 160/3; 181/1; 204/1; 252/2; 279/2; 306/3	A;Introns: 34/1; 6/0/2; 98/1; 145/3; 160/3; 181/1; 204/1; 252/2; 279/2; 306/3	
Db	14 LILSTFTYLLFGAMVFDKL-----SERKDTWVRDETERITDRKLHK-YNFSRDL--LHL 64	Query Match Score 286.5; DB 2; Length 334;	Query Match Score 286.5; DB 2; Length 334;	
Qy	107 VAAINAGIIPLGNSNSNOVSH-WDLGSSEFFAGTVTTTIGFMNISPRTEGGKIFCITYALL 165	Best Local Similarity 28.7%; Pred. No. 1.3e-15;	Best Local Similarity 28.7%; Pred. No. 1.3e-15;	
Db	50 IFLVVVYLIGAAVFKALEQFOEISORTTIV--IOKOTFIAQHACVNSTELDELJQQI 106	Matches 90; Conservative 58; Mismatches 113; Indels 53; Gaps 12;	Matches 90; Conservative 58; Mismatches 113; Indels 53; Gaps 12;	
Qy	50 IFLVVVYLIGAAVFKALEQFOEISORTTIV--IOKOTFIAQHACVNSTELDELJQQI 106	A;Molecule type: DNA	A;Molecule type: DNA	
Db	65 FEAAIAKSIPI----QQAGYQWQFQAFAYFATVVTITVGHISAPSNTAGKLFCMIPAL 119	A;Accession: T23182	A;Accession: T23182	
Qy	166 GIPLGFPLLAGVGDQLTGFKGLAKVBDTFIK-----WAVNSQTKRIIS-TIIFLFG 218	A;Status: preliminary; translated from GB/EMBL/DDJB	A;Status: preliminary; translated from GB/EMBL/DDJB	
Db	120 GVPGLIMFQSGTGERVNTFIAYSLHLHQGFTCLOQBTPTPHLMLMSLTIGFNV--177	A;Residues: 1-383 <WIL>	A;Residues: 1-383 <WIL>	
Qy	219 CVLFVALPAVIFKHIEGMSALDAIYFVVTUTLTFGDDYVA-----WAVNSQTKRIIS-TIIFLFG 218	A;Cross-references: UNIPROT:Q21094; EMBL:275543; PIDN:CAA99871.1; GSPDB:GN00023; CESP:KO	A;Cross-references: UNIPROT:Q21094; EMBL:275543; PIDN:CAA99871.1; GSPDB:GN00023; CESP:KO	
Db	178 -----IVSGTYMEHTIERTWSIIPAYFCMITSIGFDTLVLQVNLQDQPLYVFTAM 233	A;Experimental source: clone K01D12	A;Experimental source: clone K01D12	
Qy	277 WILVGLAYFAAVLSMIGDWLRLVISKKTKTKEEYGEFRAAETANTVTAEFKETRRRLSVEI 336	C;Genetics:	C;Genetics:	
Db	234 FLIGLAVFSACVNTL-----VLFGMASNADEVTA-----AQREPPSAIV 273	A;Gene: CESP:K01D12.4	A;Gene: CESP:K01D12.4	
Qy	337 YDKFPLRATSVRKL 350	A;Map Position: 5	A;Map Position: 5	
Db	274 LERFTTRANSVDSQI 287	A;Introns: 28/3; 76/3; 184/2; 217/2; 270/2; 295/2	A;Introns: 28/3; 76/3; 184/2; 217/2; 270/2; 295/2	
Qy	15 NSKPRLSKSSPKTFLASRVESDAINYMKWTVSTIPLVWVYXLIIGAVFKALEQOEI 74	Query Match Score 289; DB 2; Length 383;	Query Match Score 289; DB 2; Length 383;	
Db	1.9 NTLPSTIRAKVGCPARLIVYEENARFV-----ICILIVLAFLGQILFHWENEV 71	Best Local Similarity 24.2%; Pred. No. 9.2e-16;	Best Local Similarity 24.2%; Pred. No. 9.2e-16;	
Qy	75 SQRTTI---VIQKOTPIQHACVNSTELDELIQIVAAINAGITPLGNSNSQVSHWDLGS 131	Mismatches 80; Conservative 80; Mismatches 122; Indels 74; Gaps 14;	Mismatches 80; Conservative 80; Mismatches 122; Indels 74; Gaps 14;	
Db	72 DERIAIDNRMADYQKVYKHKPLNECDDEEMYRFISDGATSGHL---NSRSRFDH--LG- 125	RESULT 8	RESULT 8	
Qy	132 SPPFAGTTTIGFGNISPRTEGKIFLIIYALLG---IPDFGFLLAGVGQQLGTIPKG 187	T43361	T43361	
Db	126 SLFSSATVISTIGFGTSSPRTHLGRFITIVGVGCTCIVLFLNLFU---ERLVIGMSY 181	C;Species: Caenorhabditis elegans	C;Species: Caenorhabditis elegans	
Qy	188 GIAKVDETFIKWNVSQTKRIIS-TIIFLFG-----FILFG-C 219	C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004	C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004	
Db	182 ILLSLREKIRYRIKESNKPVTLUNNEDFNSSSSCGGMNDWRPSVVKYFVFLSMC 241	R;Wang, Z.W.; Salkoff, L.	R;Wang, Z.W.; Salkoff, L.	
Qy	220 VLFPVALPPAVIFKHIEGMSALDAIYFVVTUTLTFGDDYVAGSSDIEYL-DEYKPVVWF 277	A;Description: Potassium channels in C. elegans	A;Description: Potassium channels in C. elegans	
Db	244 LVLLITASGIYSVENNNYIDSLYFCIPSATGCFYVSQDVTMRSPDLYRFVNFCI 301	A;Reference number: 222450	A;Reference number: 222450	
Qy	220 VLFPVALPPAVIFKHIEGMSALDAIYFVVTUTLTFGDDYVAGSSDIEYL-DEYKPVVWF 277	A;Accession: T43361	A;Accession: T43361	
Db	244 LVLLITASGIYSVENNNYIDSLYFCIPSATGCFYVSQDVTMRSPDLYRFVNFCI 301	A;Status: preliminary; translated from GB/EMBL/DDJB	A;Status: preliminary; translated from GB/EMBL/DDJB	
Qy	220 VLFPVALPPAVIFKHIEGMSALDAIYFVVTUTLTFGDDYVAGSSDIEYL-DEYKPVVWF 277	A;Molecule type: mRNA	A;Molecule type: mRNA	
Db	244 LVLLITASGIYSVENNNYIDSLYFCIPSATGCFYVSQDVTMRSPDLYRFVNFCI 301	A;Residues: 1-364 <WAN>	A;Residues: 1-364 <WAN>	

A; Cross-references: UNIPROT:O76790; EMBL:AF03646; PIDN: AAC32857.1	Db	281	---PIVGVLILLIGSLIVSTVMTLIIQQIBALASSMKNDIQEYARALNEAREDEVDEH	336
Query Match	Qy	13 -7%	Score 28.6 ; DB 2 ; Length 364;	
Best Local Similarity	C:Species: Caenorhabditis elegans	28.7% ; Pred. No. 1.4e-15 ; Matches 58 ; Mismatches 113 ; Indels 53 ; Gaps 12;		
Matches 90 ; Conservative	C:Accession: T43394			
Qy	Db	50	IPLVUVLYLIGAAVKALEQDQEISQRTTV--IQQTPIAQAHACVNSTELDIQI	106
Qy	Db	14	LILSTFTYLFGAMVFDKLE----SEKDWTVRDDEERITDRLKEK-YNSFED--LHL	64
Qy	Db	107	VAAINAGI1PLGNSSNOVSH-WDLGSFFAGTGVTTGFGNISPRTEGGKIFCIIYALI	165
Qy	Db	65	PEIAIKSIP----QAGIOWQFAGAFYATVVITVGGHSASTNAGLFCMIAFL	119
Qy	Db	166	GIPLFGLPLLAGVGDQLGTIFGKGIAKVDETPIK---KNSQTKIRIIS-TIIFLFG	218
Qy	Db	120	GVPVGMJMFQSGTVERNTFIAYSLHKFRDSLHQOGFTCLQEVTPTHLLMSLTIGFMV-	177
Qy	Db	219	CVLVALPAVIFRHLLEGWSALDAIYFVVTIITTGFDYV--AGSSDIEIYLDFTYKPVVWF	276
Qy	Db	178	---IVSGTVMNHTIEKWSIIDAYFCMITSFESTIYFGDLYPLQVNTNALQDQPLYWYFATIM	233
Qy	Db	277	WILGLAYFAAVLMSIGDWLRVSKTKTEKEYGEFRAHAEMTANVTAEFKETRRLSVEI	336
Qy	Db	234	FILIGAVFSACVNLI-----VLFGMASNADDEVA-----AQREPPSAIV	273
Qy	Db	337	YDKFQFATSVRKLI	350
Qy	Db	274	LERFTENSLVDSQI	287
RESULT 9				
T43394	Db	74	potassium channel chain n2P18 homolog - Caenorhabditis elegans	
C; Species: Caenorhabditis elegans	C:Accession: T43394			
C; Date: 21-Jan-2000 #sequence_revision 21-Jan-2000	C:Accession: T43394	#text_change 09-Jul-2004		
R; Kunkel, M.T.; Salkoff, L.				
A; Description: Potassium channels in C. elegans.				
A; Reference number: Z22479				
A; Accession: T43394				
A; Status: preliminary; translated from GB/EMBL/DDBJ				
A; Molecule type: mRNA				
A; Residues: 1-61 <KUN>				
A; Cross-references: UNIPROT:Q18120; EMBL:AF083650; PIDN: AAC328561.1				
Query Match	Qy	13 -4%	Score 279.5 ; DB 2 ; Length 461;	
Best Local Similarity	C:Species: Caenorhabditis elegans	23.5% ; Pred. No. 6.8e-15 ; Matches 70 ; Mismatches 133 ; Indels 129 ; Gaps 14;		
Matches 102 ; Conservative	C:Accession: T45032			
Qy	Db	46	TVSTIP-----LVVVLYLIGAAVKALEQEISQRTTIVIQKOTFIQAHACTV	95
Qy	Db	10	TILTIPQRTFKGQPLLIVAYTLGAWIWMIEGENE--REMIEQK-----	56
Qy	Db	96	STELDELIQVIAAIN-----AGIPLGNSSNOVS	125
Qy	Db	57	--ERDLSRRTYKCNQQLQIKQRORRIMTAEYNRKTAVLTTFQETLGIVPA--DMDKDI	112
Qy	Db	126	HWDLGSSFFAGTVTIGFGNISPRTEGGKIFCIIYALIIGLPIFLLAGVGDOLGTIF	185
Qy	Db	113	HWTFLGSFISFYCMVTTGNGNIVPCTGWGRFATIYAFIGPLTVLSY--CLGSUF	168
Qy	Db	186	GKGIAKVDTEPKWNSQTKIRIIS---	210
Qy	Db	169	ARGCMLWRFPLK-----STRVSDLKNKISEADNNBEGTAITPSAKTEKTNDDL	222
Qy	Db	211	--TIFLFGCVLVALPAVIEKHEGWSALDAIYFVVTIITTGFDYVAGGSDIEYL	267
Qy	Db	223	LSFPFSLGSLIITVIVNIFCAVLTFLFEWDRGTSLYFTLSIFTGQDILP--SDYDFPM	280
Qy	Db	268	-----DFYKPVVFWLVLGGLAYPAAVLSMCDWLRVISKEVGEFRAH-----AEWTAN	320
RESULT 11				
T45032	Db	1	hypothetical protein Y99B6.f [imported] - Caenorhabditis elegans	
C; Species: Caenorhabditis elegans	C:Accession: T45032			
C; Date: 21-Jan-2000 #sequence_revision 21-Jan-2000	C:Accession: T45032	#text_change 21-Jul-2000		
R; Wilson, R.; Ainscough, R.; Anderson, K.; Baynes, C.; Berks, M.; Borfield, J.; Burton, A.; Fulton, L.; Hawkins, T.; Hillier, L.; Jier, M.; John B.; O'Callaghan, M.; Parsons, J.; Percy, C.; Roopra, A.; Saunders, D.				
Nature 358, 32-38, 1994				
A; Authors: Showkeen, R.; Sims, M.; Smalldon, N.; Smith, A.; Smith, M.; Sonnhammer, E.; Stoeck, L.; Wilkinson-Sprout, J.; Wilson, P.				
A; Title: 2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans				

A; Reference number: S43531; MUID:94150718; PMID:7906398  
 A; Accession: T45032  
 A; Status: preliminary; translated from GB/EMBL/DBJ  
 A; Molecule type: DNA  
 A; Residues: 1-392 <WIL>  
 A; Cross-references: EMBL:ALI32896; NID:96134440; PIDN:CAB60911.1; PID:96434446  
 A; Experimental source: clone Y39B6B  
 C; Genetics:  
 A; Map position: 3  
 A; Intron: 82/2 : 106/3 ; 151/1 : 220/1 ; 260/3 : 370/3  
 A; Note: Y39BB.£

Query Match 13.0% Score 271; DB 2; Length 392;  
 Best Local Similarity 25.8%; Pred. No. 2.7e-14;  
 Matches 82; Conservative 65; Mismatches 109; Indels 62; Gaps 12;

Qy 7 LDPKSAAGNS----KPRLSFSKKPTVILAS---RVEESDAINVMKMKTVSTIFLVVWLY 57  
 Db 64 LEPRTSAAHSSSLYPVEPPKMAIAKEMSFSDQKLPKFFPSLKSICLKPAQRY---- 117

Qy 58 LITGAAVFKALEQPQEISORTTIVQKQTPIAQ -HACVNSTEDELQI-QI-VAAINNGI 114  
 Db 118 -----FSRIEPPLEKIERAEVDYDQNQWRDLIQLIDSEEDSKLFLNIREAALNG-- 168

Qy 115 IPIGNSSNQVSHWDLGSSFFAGTVITTCGFTNTSPTEGGFTNITALLGIPLFGRFL 174  
 Db 169 IWDRLNLSDPNTTFQGQAFFAGTLLSTVGYGRSPBYGKFTILCVIGPLTLALL 228

Qy 175 AGV-----GDQLGTTFGKGIAKYBDTPKWNYSQTKIRIISTTIFLFGC 219  
 Db 229 SALVARMEPSPHKLRLGLNORLGHFL-----TVNHICLHYGV-VPASL 271

Qy 220 VLFY-ALPAVIFKHIE-GHSALDAIYFVVTITLGFDYVAGGS-DIBYLDYKPVVWF 276  
 Db 272 LLFWFAIAFWVSEETDSYSLDAFYCCEVSLTTGCDPEPDDPNQSFRGLYKIGATV 331

Qy 277 WILGLAYFAAVLSMIGD 294  
 Db 332 YLMGGLCCNMFLFLATLYD 349

RESULT 1.2  
 T24265 hypothetical protein T01B4.1 - Caenorhabditis elegans  
 C; Species: Caenorhabditis elegans  
 C; Accession: T24265  
 R; Wilkison, J.  
 A; Reference number: Z19866  
 A; Molecule type: DNA  
 A; Residues: 1-522 <WIL>  
 A; Cross-references: UNIPROT:Q22042; EMBL:270036; PIDN:CAA93875.1; GSPDB:GN00028; CESP:T01B4  
 A; Experimental source: clone T01B4  
 C; Genetics:  
 A; Gene: CESP:T01B4.1  
 A; Map position: X 95/3 : 142/1 ; 224/3 ; 290/1 ; 458/1  
 Query Match 12.9% Score 270.5; DB 2; Length 522;  
 Best Local Similarity 23.7%; Pred. No. 4.2e-14;  
 Matches 102; Conservative 64; Mismatches 136; Indels 129; Gaps 15;

Qy 50 IFLVVVLITLIGAAVPALEQPKQFQ-----ISOPTTIVQKQPFIAQHACVNSTE 98  
 Db 41 LILILGVALGGMQALEYDQOOLEFAEKVRLRSSLLAVNLLEHLKQMNCQSQNE 100

Qy 99 LDELIQQTAAINGIIPIGNSS -NOVSEHWDLGSSFPFAGTVITTGFGNISPRTEGGKI 157  
 Db 101 -----KRCLDELTTRPIORSDEERGEGNRWDFNSVFSATIPTTIGGNLACKTNLGR 155

Qy 158 FCTIYALIJGIPLFGFLLLAGVGVD-----OLGGTIFGKG 188  
 Db 156 ATIVGMMGIPMLFVKLNFGELCKRKCRGKOKRASSLASITSKE 215

Qy 189 IAKY-----BDTF - IKNNVSQTKIRIISTTIFLFGCVLFLVALPAVFKHIEGWS 237  
 Db 216 MLEVFVFEVPEPDDEKDFTFQLRNG-----LLVTVLFWVLCFSFWENWD 260

Qy 238 ALDAIYFVVITLTIGFDYVAGGSDBIYLDYKPVVWFIL -WGLAYFAAVLSMIGD- 294  
 Db 261 PLTAPYFFEVSLSTIGFSDIVP-----DHPIRACALFVLYFQIGLAFAMVYALQER 312

Qy 295 -----W-LRVSKTKEBEVGFRAHAETWANT----- 322

Db 313 VENQYMMALLELDQKIQSKLQDMYDEDEKKADKNDMHPFSKKEPVVRGPRLQDLRGPD 372

Qy 323 AEEFKETRRRLS----VBIYDKFQRTATSVKRKLSAEL-----AGHNHOELTPCRTTLS 370  
 Db 373 LKISGGERSSDASVTEASDTRHEKVGRAILABAFAFDRASNGHTQLNCS--Tvs 430

Qy 371 VHLLTSEREVL 381

Db 431 NEHDSCQTEAI 441

RESULT 1.3  
 T15584 hypothetical protein C24A3.6 - Caenorhabditis elegans  
 C; Species: Caenorhabditis elegans  
 C; Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
 C; Accession: T15584  
 R; Favell, T.  
 Submitted to the EMBL Data Library, November 1995  
 A; Description: The sequence of C. elegans cosm id C24A3.  
 A; Accession: T15584  
 A; Status: preliminary; translated from GB/EMBL/DDBJ  
 A; Molecule type: DNA  
 A; Residues: 1-325 <FAV>  
 A; Cross-references: EMBL:040424; NID:91065543; PIDN:AAA81455.1; PIDN:AAA81455.1; CESP:C24A3.6  
 A; Gene: CESP:C24A3.6  
 A; Introns: 21/1; 63/3; 131/1; 193/3; 206/3  
 Query Match 12.9% Score 269; DB 2; Length 325;  
 Best Local Similarity 25.4%; Pred. No. 3.2e-14;  
 Matches 87; Conservative 53; Mismatches 87; Indels 116; Gaps 11;

Qy 46 TVSTIF-----LIVWLYLIGAAVFKALEQPOPIOSQTTIVQKQTFLAQHACVN 95  
 Db 10 TILTFTQKTFKGFLPLILVAVTLLGAWIFWMIEGENE--REMILHQK----- 56

Qy 96 STELDLDELQIQVAAIN-----AGIIIPLGNSSNQVS 125  
 Db 57 --ERBDLIRRTRYKINOLQIKHQRLTAEEYNTARTKLTVFQBTGIVPA--DMDKDI 112

Qy 126 HDLGLSSPPFACTVITTGFGKISPRTEGGKIFCITYALLGIPFGFLLAGVGDQLSTIF 185  
 Db 113 HWTFLGSIFYCMVYTITGYGNIVPGTGWGRPATILYAFIGPLTVLSY---CLGSLF 168

Qy 186 GKGIKAYVEDTFIKWNVSQTKIRIIS-----STRVSKDLSNKISEADNIEGTTATPSAETENNDL 222

Db 169 AKCCKMLWRFELK----- 21.0

Qy 211 ---TIIIFLFGCVLFLVALPAVFKHIEGWSALDAIYFVVITLTIGFGDYVACGSDIEYL 267  
 Db 223 LSFPISGHLITVWIFCAVLFELBMDFTSFLYTLISFTIGFDILP--SDYDFM 280

Qy 268 DFKPKPVVWFILVGLAYFAAVLSMIGDMLRVS-----KKTKR 305  
 Db 281 -----PIVGVLILJGLSLVSTVWLIQQQIEALASVRRKCK 319

RESULT 14

H88124 protein T12C9.3 [imported] - *Caenorhabditis elegans*  
 C;Species: *Caenorhabditis elegans*  
 C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 10-May-2001  
 C;Accession: H88124  
 R;Anonymous, The *C. elegans* Sequencing Consortium.  
 Science 282, 2012-2018, 1998  
 A;Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biology  
 A;Reference number: A75000; PMID:99069613; PMID:9851916  
 A;Note: see websites genome.wustl.edu/gsc/elegans/ and www.sanger.ac.uk/Projects/C\_elegans/  
 A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and  
 A;Accession: H88124  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-110 <STO>  
 A;Cross-references: GB:chr\_II; PIDN:AC71141.1; PID:gi1086770; GSPDB:GN00020; CESP:T12C9.3  
 A;Proline-rich  
 A;Genetics:  
 A;Gene: T12C9.3  
 A;Map position: 2

Query Match 12.7%; Score 266; DB 2; Length 1910;  
 Best Local Similarity 22.9%; Pred. No. 4 6e-13;  
 Matches 102; Conservative 71; Mismatches 127; Indels 146; Gaps 17;

Qy 18 PRSL-TSSKPRVTLASRVSDSAI-INVKWKTYSTTIFVVV---LYLJIGAAVEKA 67  
 Db 162 PQFSRRSFISPGILESARPDDETTTLQNIRKTYAKALPHIVLVVVCVITATGAWIFT 221

Qy 68 LEQPQE--ISQRTTIVIQKQTPIAQHACUNSTELD-BLI-----Q 104  
 Db 222 LESPNEDRKLKEPKRTIAEMSNLVI-INNEKEVWKEDIEKLMYSEKLYKAFKE 278

Qy 105 QIVAAINGIPL-----GNSNOVSH-----MDLGSSFFAG 137  
 Db 279 QVRYSDVRTIGPEGRASSYYEADETGDSERIKRHRHGKRGDRGSEKWWTTSSALFRA 338

Qy 138 TWTTTIGGNISPRTEGGSKFCIYLAIAGIPLFGELIAGVGDOLG-TIF----GKGIA 190  
 Db 339 TTMATIGGNIVBVTPLGRLAIVLFAFPAAITIGDLGRFLSCTIWYKMRKGSA 398

Qy 191 KVDTFIKW-----NVYSQTKIRIISTIIFILFGCV 220  
 Db 399 RLSAWKFERGLGELDISBDDLESASKNODISSILDMDDBIDSEVPVLMFTI-----L 452

Qy 221 LFVALPAVIFKIGHEGWSALDAYFVWVLTIGFQDGYAGGSDEIYDFYKPVVWWFLV 280

Db 453 LYTAFGGILFLSILEDWSMADFYSFISLTTIGFGD.IVOPENHD----YIAIMLILGV 506

Qy 281 GLAYFRAAVLMSIG------DWLURVISKTKT-----EVGEFRAH 313

Db 507 GLSVTTMCGIDLACIQYTORIHYFGRKFQGTDLQYLKKRMDERLLAMGQGBEILRKYVH 566

Qy 314 AABWTANTAAFEKTRRRLSVEYDK 339  
 Db 567 AYE-----KPEREQSGLQQRMEE 585

A;Experimental source: clone F19D8  
 C;Genetics:  
 A;Map position: X  
 A;Introns: 31/1; 82/2; 101/3; 157/1; 197/1; 230/3; 267/2; 325/3; 356/1; 404/3  
 Query Match 12.6%; Score 263; DB 2; Length 452;  
 Best Local Similarity 29.3%; Pred. No. 1.4e-13;  
 Matches 86; Conservative 52; Mismatches 124; Indels 32; Gaps 9;  
 Qy 32 RVESSDAINTMKWKVSTI-----FLVFLYLIGAAYPKALEQPKQEI---SQRRTI 80  
 Db 26 KLKCNISKCAMMKFERNVLRALGHLLYCPVVCYVFAGAWYFHOLEGENETELHDQREVA 85  
 Qy 81 VIOQKOTFIAOHACV-NSTELDELQCOVAAINRGLIPLG----NSSNOV--SHWDLGS 132  
 Db 86 MNLKCDVIAKLAATTENAEINEHLMFLRNINSNLISLDNYLIFNEPTQIVPKRTTPSS 145  
 Qy 133 PPFAGTVITIGEGNISPRTEGGKIPFCITYALLGIPLFGLLLAGYDOLGTIFGKGIAKY 192  
 Db 146 VLFSPTILITIGYGNVTPHQCKPLMTYGAFLGFLITIADGFRSKTAIMALVQKV 205  
 Qy 193 EDTFIKWNVSQTKIRIISTI--IFILFGCVLFVLPAPVFKHIGW--SALDAIFIYV 245  
 Db 206 SKREKKQSDEHLLEBIAEVSPYLDVLLVAGLFVVFIAIGSAVFLWENQLTYFFSVYFS 265  
 Qy 246 VITLTIGFGDYVAGGSDDIEYDFYKPVVWWFLVYGLAYPAAVLGMIDGMWLRVI 299  
 Db 266 YMSLTITGLDIVP----RMDMFLPLTLYITIGLWLTTALVEQLADVFLV 313

Search completed: July 13, 2005, 08:45:42  
 Job time : 23.6316 secs

## RESULT 15

T21118 hypothetical protein F19D8.1 - *Caenorhabditis elegans*  
 C;Species: *Caenorhabditis elegans*  
 C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
 C;Accession: T21118  
 R;Swinburne, J.; Ainscough, R.  
 Submitted to the EMBL Data Library, August 1996  
 A;Reference number: Z19377  
 A;Accession: T21118  
 A;Status: preliminary; translated from GB/EMBL/DDJB  
 A;Molecule type: DNA  
 A;Residues: 1-452 <STO>  
 A;Cross-references: UNIPROT:Q93531; EMBL:278541; PIDN:CAB01740.1; GSPDB:GN00028; CESP:F1

Result No.	Score	Query Match	Length DB	ID	Description
1	2084	99.7	411	9	US-09-828-746-6 Sequence 6, Appli
2	2044	97.8	411	9	US-09-828-746-6 Sequence 2, Appli
3	2044	97.8	411	14	US-10-121-746-83 Sequence 83, Appli
4	2044	97.8	411	16	US-10-145-21-2 Sequence 2, Appli
5	2044	97.8	411	16	US-10-349-528-31 Sequence 31, Appli
6	2044	97.8	411	17	US-10-916-644-83 Sequence 83, Appli
7	2044	97.8	411	17	US-10-916-647-83 Sequence 93, Appli
8	2041	97.7	411	11	US-09-828-360-18 Sequence 18, Appli
9	2038	97.5	422	16	US-10-349-528-20 Sequence 20, Appli
10	2011	96.2	426	8	US-08-816-011-45 Sequence 45, Appli
11	2011	96.2	426	17	US-10-870-492-45 Sequence 45, Appli

RESULT 2

Qy 61 GAAVFKALEQPBISORTTIVQKQRTIAQACVNSTELDELIQQVAAINAGIIPGNS 120  
 Db 121 SNOVSHWDLGSSPFAGTTTIGFGNISPRTEGGKFCITIALLGIPFGPLLGVGDQ 180  
 Qy 121 SNOVSHWDLGSSPFAGTTTIGFGNISPRTEGGKFCITIALLGIPFGPLLGVGDQ 180  
 Db 181 LGTFKGKIAKVEDTFIKWNVSOTKIRIISTIIFLGCVLVALPAVIFKHIEGSALD 240  
 Qy 181 LGTFKGKIAKVEDTFIKWNVSOTKIRIISTIIFLGCVLVALPAVIFKHIEGSALD 240  
 Db 181 LGTFKGKIAKVEDTFIKWNVSOTKIRIISTIIFLGCVLVALPAVIFKHIEGSALD 240  
 Qy 241 AYFVVITLTIGFGDYAGGSDEIYLDFYKVWWFLVGLAYFAAVLSMIGDWLRVIS 300  
 Db 241 AYFVVITLTIGFGDYAGGSDEIYLDFYKVWWFLVGLAYFAAVLSMIGDWLRVIS 300  
 Qy 301 KTKKEVGEFHAAEWTANTAEFKTRRSLSEIYDKFORATSVRKLSAELAGHNQ 360  
 Db 301 KTKKEVGEFHAAEWTANTAEFKTRRSLSEIYDKFORATSVRKLSAELAGHNQ 360  
 Qy 361 ELTPCRTLTSVNLTSEREVPLPLKTESIYLNGLTPHCAEDIAVENMK 411  
 Db 361 ELTPCRTLTSVNLTSEREVPLPLKTESIYLNGLTPHCAEDIAVENMK 411  
 Qy 361 ELTPCRTLTSVNLTSEREVPLPLKTESIYLNGLTPHCAEDIAVENMK 411  
 Db 361 ELTPCRTLTSVNLTSEREVPLPLKTESIYLNGLTPHCAEDIAVENMK 411

RESULT 3

Qy 301 KTKKEVGEFHAAEWTANTAEFKTRRSLSEIYDKFORATSVRKLSAELAGHNQ 360  
 Db 301 KTKKEVGEFHAAEWTANTAEFKTRRSLSEIYDKFORATSVRKLSAELAGHNQ 360  
 Qy 361 ELTPCRTLTSVNLTSEREVPLPLKTESIYLNGLTPHCAEDIAVENMK 411  
 Db 361 ELTPCRTLTSVNLTSEREVPLPLKTESIYLNGLTPHCAEDIAVENMK 411  
 Qy 361 ELTPCRTLTSVNLTSEREVPLPLKTESIYLNGLTPHCAEDIAVENMK 411  
 Db 361 ELTPCRTLTSVNLTSEREVPLPLKTESIYLNGLTPHCAEDIAVENMK 411

Query Match 97.8%; Score 2044; DB 14; Length 411;  
 Best Local Similarity 96.4%; Pred. No. 3.5e-185;  
 Matches 396; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MAAPDLDPKSAQNSKPKLSSKPTVLASRVESDSAINUMKWTYSTIPLVWVYLII 60  
 Db 1 MAAPDLDPKSAQNSKPKLSSKPTVLASRVESDSAINUMKWTYSTIPLVWVYLII 60  
 Qy 61 GRAVIAKALEQPKBISORTTIVQKOPTIAQACVNSTELDELIQVAAINAGIIPGNS 120  
 Db 61 GRAVIAKALEQPKBISORTTIVQKOPTIAQACVNSTELDELIQVAAINAGIIPGNS 120  
 Qy 61 GATVFKALEQPKBISORTTIVQKOPTISQHCVNSTELDELIQVAAINAGIIPGNT 120  
 Db 61 GATVFKALEQPKBISORTTIVQKOPTISQHCVNSTELDELIQVAAINAGIIPGNT 120

Query Match 97.8%; Score 2044; DB 14; Length 411;  
 Best Local Similarity 96.4%; Pred. No. 3.5e-185;  
 Matches 396; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MAAPDLDPKSAQNSKPKLSSKPTVLASRVESDTINTMKWTYSTIPLVWVYLII 60  
 Db 1 MAAPDLDPKSAQNSKPKLSSKPTVLASRVESDTINTMKWTYSTIPLVWVYLII 60  
 Qy 121 SNOVSHWDLGSSPFAGTTTIGFGNISPRTEGGKFCITIALLGIPFGPLLGVGDQ 180  
 Db 121 SNOVSHWDLGSSPFAGTTTIGFGNISPRTEGGKFCITIALLGIPFGPLLGVGDQ 180  
 Qy 181 LGTFKGKIAKVEDTFIKWNVSOTKIRIISTIIFLGCVLVALPAVIFKHIEGSALD 240  
 Db 181 LGTFKGKIAKVEDTFIKWNVSOTKIRIISTIIFLGCVLVALPAVIFKHIEGSALD 240  
 Qy 241 AYFVVITLTIGFGDYAGGSDEIYLDFYKVWWFLVGLAYFAAVLSMIGDWLRVIS 300  
 Db 241 AYFVVITLTIGFGDYAGGSDEIYLDFYKVWWFLVGLAYFAAVLSMIGDWLRVIS 300  
 Qy 301 KTKKEVGEFHAAEWTANTAEFKTRRSLSEIYDKFORATSVRKLSAELAGHNQ 360  
 Db 301 KTKKEVGEFHAAEWTANTAEFKTRRSLSEIYDKFORATSVRKLSAELAGHNQ 360  
 Qy 361 ELTPCRTLTSVNLTSEREVPLPLKTESIYLNGLTPHCAEDIAVENMK 411  
 Db 361 ELTPCRTLTSVNLTSEREVPLPLKTESIYLNGLTPHCAEDIAVENMK 411

RESULT 4

US-10-745-2210-2  
; Sequence 2, Application US/10745210  
; Publication No. US20040143855A1  
; GENERAL INFORMATION:  
; APPLICANT: TONONI, Giulio  
; ATTORNEY OR AGENT: CIRELLI, Chiara  
; TITLE OF INVENTION: ION CHANNELS AS TARGETS FOR SLEEP-RELATED DRUGS  
; CURRENT APPLICATION NUMBER: US/10/745,210  
; FILE REFERENCE: 054030-0044  
; CURRENT FILING DATE: 2003-12-23  
; PRIOR APPLICATION NUMBER: US 60/436,201  
; PRIOR FILING DATE: 2001-12-23  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2  
; LENGTH: 411  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-745-2210-2

Query Match 97.8%; Score 2044; DB 16; Length 411;  
Best Local Similarity 96.4%; Pred. No. 3\_5e-185;  
Matches 396; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MAAPDLIDPKSAQNSKPLRSKPTVLASRVSDAINVMWKVTSIFLVVVLII 60  
Db 1 MAAPDLIDPKSAQNSKPLRSKPTVLASRVSDTINVMWKVTSIFLVVVLII 60

Qy 61 GAAVKALEQQPQISORTTIVIQKQTPIAQHACVNSTELDELIQIVAAINAGIPLGNS 120  
Db 61 GATVFKALEQPHEISORTTIVIQKQTFSQHSCVNSTELDELIQIVAAINAGIPLGNT 120

Qy 121 SNQISHWDLGSSPFAGTTTIGFGNISPRTEGGKFCIYALLGIPLGFLAGVGDQ 180  
Db 121 SNQISHWDLGSSPFAGTTTIGFGNISPRTEGGKFCIYALLGIPLGFLAGVGDQ 180

Qy 181 LGTFGKGIAKVEDFTIKWNVSOTKIRIISTIIFLFGCVLFWALPAVIFKHIEGWSALD 240  
Db 181 LGTFGKGIAKVEDFTIKWNVSOTKIRIISTIIFLFGCVLFWALPAVIFKHIEGWSALD 240

Qy 241 AIVFVITLTIGFGDYAGGSDEIYLDFYKPVWFWTLVGLAYFAAVLSMIGDWLRVIS 300  
Db 241 AIVFVITLTIGFGDYAGGSDEIYLDFYKPVWFWTLVGLAYFAAVLSMIGDWLRVIS 300

Qy 301 KCTKEEVGBFRAHAETWNTAEKFETRRLSVBIDDKFORATSVKRLSABLAGHNQ 360  
Db 301 KCTKEEVGBFRAHAETWNTAEKFETRRLSVBIDDKFORATSVKRLSABLAGHNQ 360

RESULT 6  
US-10-745-2210-3  
; Sequence 3, Application US/10976644  
; Publication No. US20050112662A1  
; GENERAL INFORMATION:  
; APPLICANT: Miller, Andrew P., Curran, Mark Edward  
; ATTORNEY OR AGENT: Hu, Ping  
; APPLICANT: Rutter, Marc  
; APPLICANT: Wang, Jian-Wang  
; TITLE OF INVENTION: Novel Human Potassium Channel 6  
; FILE REFERENCE: SEQ-15P  
; CURRENT APPLICATION NUMBER: US/10/976,644  
; PRIOR APPLICATION NUMBER: US/09/336,643  
; PRIOR FILING DATE: 1999-06-18  
; PRIOR APPLICATION NUMBER: 60/076,687  
; PRIOR FILING DATE: 1998-08-07  
; PRIOR APPLICATION NUMBER: 60/116,448  
; PRIOR FILING DATE: 1999-01-19  
; PRIOR APPLICATION NUMBER: PCT/US99/03826  
; NUMBER OF SEQ ID NOS: 87  
; SEQ ID NO 83  
; TYPE: PRT  
; ORGANISM: H. sapiens  
; US-10-745-2210-3

Query Match 97.8%; Score 2044; DB 17; Length 411;  
Best Local Similarity 96.4%; Pred. No. 3\_5e-185;  
Matches 396; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MAAPDLIDPKSAQNSKPLRSKPTVLASRVSDAINVMWKVTSIFLVVVLII 60  
Db 1 MAAPDLIDPKSAQNSKPLRSKPTVLASRVSDTINVMWKVTSIFLVVVLII 60

RESULT 5  
US-10-349-528-31  
; Sequence 31, Application US/10349528  
; Publication No. US20040253668A1  
; GENERAL INFORMATION:  
; APPLICANT: RAMANATHAN, Chandra  
; ATTORNEY OR AGENT: Gopal, Shuba  
; APPLICANT: Mintier, Gabe  
; APPLICANT: Feder, John  
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR (GPCR) VARIANTS AND METHODS OF FILE REFERENCE: D0210  
; CURRENT APPLICATION NUMBER: US/10/349,528  
; CURRENT FILING DATE: 2003-01-22  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 31  
; LENGTH: 411  
; TYPE: PRT  
; ORGANISM: HOMO SAPIENS

61 GAAVFKALEQPOEISORTIVIQQQTIAQHACVNSTELLIQIVAAINAGIPLGNS 120  
 61 GATVFKALEQPHISORTIVIQQQTISQVSCVNSTELLIQIVAAINAGIPLGNT 120  
 Db 61 SNOQSHWDLGSSPFFACTVITIGFGNISPRTEGGKFCITYALIGIPLFGFLAVGVDQ 180  
 Qy 121 SNOQSHWDLGSSPFFACTVITIGFGNISPRTEGGKFCITYALIGIPLFGFLAVGVDQ 180  
 Db 121 SNOQSHWDLGSSPFFACTVITIGFGNISPRTEGGKFCITYALIGIPLFGFLAVGVDQ 180  
 Qy 181 LGTIFGKGIAKYEDTFIKWNVSQTKRISTIILIFGCVLFAVPAIFKIEGSALD 240  
 Db 181 LGTIFGKGIAKYEDTFIKWNVSQTKRISTIILIFGCVLFAVPAIFKIEGSALD 240  
 Qy 181 LGTIFGKGIAKYEDTFIKWNVSQTKRISTIILIFGCVLFAVPAIFKIEGSALD 240  
 Db 181 LGTIFGKGIAKYEDTFIKWNVSQTKRISTIILIFGCVLFAVPAIFKIEGSALD 240  
 Qy 241 AIYFVVIITLTIGFDPYAGGSDFIYDLYKTRRLSVEYDKFORATSYRKLSAELGNHQ 360  
 Db 241 AIYFVVIITLTIGFDPYAGGSDFIYDLYKTRRLSVEYDKFORATSYRKLSAELGNHQ 360  
 Qy 301 KKTKEEVGEFRAHAETNTAEEKETTRRLSVEYDKFORATSYRKLSAELGNHQ 360  
 Db 301 KKTKEEVGEFRAHAETNTAEEKETTRRLSVEYDKFORATSYRKLSAELGNHQ 360  
 Qy 301 KKTKEEVGEFRAHAETNTAEEKETTRRLSVEYDKFORATSYRKLSAELGNHQ 360  
 Db 301 KKTKEEVGEFRAHAETNTAEEKETTRRLSVEYDKFORATSYRKLSAELGNHQ 360  
 Qy 361 ELTPCERTLSYNHTSEREVPLPLKAESIYLNGLTPHCAGEDIAVIENTK 411  
 Db 361 ELTPCERTLSYNHTSEREVPLPLKAESIYLNGLTPHCAGEDIAVIENTK 411  
 Qy 361 ELTPCERTLSYNHTSEREVPLPLKAESIYLNGLTPHCAGEDIAVIENTK 411  
 Db 361 ELTPCERTLSYNHTSEREVPLPLKAESIYLNGLTPHCAGEDIAVIENTK 411

RESULT 8  
 US-09-892-360-18  
 / Sequence 18, Application US/09892360  
 / Publication No. US20040101833A1  
 / GENERAL INFORMATION:  
 / APPLICANT: LAZUDSKI, MICHEL  
 / LESAGE, FLORIAN  
 / APPLICANT: ROMNEY, GEORGES  
 / TITLE OF INVENTION: HUMAN TREK2, A STRETCH-AND ARACHIDONIC ACID-SENSITIVE K+ CHANNEL ACTIVATED BY INHALATIONAL ANESTHETICS AND  
 / TITLE OF INVENTION: RILUZOLE  
 / FILE REFERENCE: 1256-B-00  
 / CURRENT APPLICATION NUMBER: US/09/892,360  
 / CURRENT FILING DATE: 2001-06-27  
 / PRIOR APPLICATION NUMBER: 60/214,559  
 / PRIOR FILING DATE: 2000-06-27  
 / NUMBER OF SEQ ID NOS: 25  
 / SOFTWARE: PatentIn Ver. 2.1  
 / SEQ ID NO 18  
 / LENGTH: 411  
 / TYPE: PRT  
 / ORGANISM: Mus musculus  
 US-09-892-360-18

Query Match 97 %; Score 2041; DB 11; Length 411;  
 Best Local Similarity 96 %; Pred. No. 6-7e-185; Indels 0; Gaps 0;  
 Matches 395; Conservative 12; Mismatches 4;

Qy 1 MAAPDLIDPKSAAQNSKPRLSFSSKPTVLASRVEDSDAINMKWTVTSTIFLVVNYLII 60  
 Db 1 MAAPDLIDPKSAAQNSKPRLSFSSKPTVLASRVEDSDTINMKWTVTSTIFLVVNYLII 60  
 Qy 61 GAAVFKALEQPOEISORTIVIQQQTIAQHACVNSTELLIQIVAAINAGIPLGNS 120  
 Db 61 GATVFKALEQPOEISORTIVIQQQTIAQHACVNSTELLIQIVAAINAGIPLGNT 120  
 Qy 121 SNOQSHWDLGSSPFAGTVTTIGFONISPRTEGGKFCITYALIPLFGFLAVGVDQ 180  
 Db 121 SNOQSHWDLGSSPFAGTVTTIGFONISPRTEGGKFCITYALIPLFGFLAVGVDQ 180  
 Qy 181 LGTIFGKGIAKYEDTFIKWNVSQTKRISTIILIFGCVLFAVPAIFKIEGSALD 240  
 Db 181 LGTIFGKGIAKYEDTFIKWNVSQTKRISTIILIFGCVLFAVPAIFKIEGSALD 240  
 Qy 241 AIYFVVIITLTIGFDPYAGGSDFIYDLYKTRRLSVEYDKFORATSYRKLSAELGNHQ 360  
 Db 241 AIYFVVIITLTIGFDPYAGGSDFIYDLYKTRRLSVEYDKFORATSYRKLSAELGNHQ 360  
 Qy 301 KKTKEEVGEFRAHAETNTAEEKETTRRLSVEYDKFORATSYRKLSAELGNHQ 360  
 Db 301 KKTKEEVGEFRAHAETNTAEEKETTRRLSVEYDKFORATSYRKLSAELGNHQ 360  
 Qy 361 ELTPCERTLSYNHTSEREVPLPLKAESIYLNGLTPHCAGEDIAVIENTK 411  
 Db 361 ELTPCERTLSYNHTSEREVPLPLKAESIYLNGLTPHCAGEDIAVIENTK 411

RESULT 9  
 US-10-976-647-83  
 / Sequence 83, Application US/10976647  
 / Publication No. US/0050112663A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Miller, Andrew P.  
 / APPLICANT: Curran, Mark Edward  
 / APPLICANT: Hu, Ping  
 / APPLICANT: Rutter, Marc  
 / APPLICANT: Wang, Jian-Wang  
 / TITLE OF INVENTION: Novel Human Potassium Channels  
 / FILE REFERENCE: SEQ-15P  
 / CURRENT APPLICATION NUMBER: US/10/976,647  
 / CURRENT FILING DATE: 2004-10-29  
 / PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/336,643  
 / PRIOR FILING DATE: CURRENT FILING DATE:1999-06-18  
 / PRIOR APPLICATION NUMBER: US/0050112663A1  
 / PRIOR FILING DATE: 1998-08-07  
 / PRIOR APPLICATION NUMBER: 60/116,448  
 / PRIOR FILING DATE: 1999-01-19  
 / PRIOR APPLICATION NUMBER: PCT/US99/038826  
 / PRIOR FILING DATE: 1999-02-22  
 / NUMBER OF SEQ ID NOS: 87  
 / SOFTWARE: Fast-SEQ for Windows Version 4.0  
 / SEQ ID NO 83  
 / LENGTH: 411  
 / TYPE: PRT  
 / ORGANISM: H. sapiens  
 US-10-976-647-83

Query Match 97.8%; Score 2044; DB 17; Length 411;  
 Best Local Similarity 96.4%; Pred. No. 3.5e-185; Indels 0; Gaps 0;  
 Matches 396; Conservative 11; Mismatches 4;

Qy 1 MAAPDLIDPKSAAQNSKPRLSFSSKPTVLASRVEDSDAINMKWTVTSTIFLVVNYLII 60  
 Db 1 MAAPDLIDPKSAAQNSKPRLSFSSKPTVLASRVEDSDTINMKWTVTSTIFLVVNYLII 60  
 Qy 61 GAAVFKALEQPOEISORTIVIQQQTIAQHACVNSTELLIQIVAAINAGIPLGNS 120  
 Db 61 GATVFKALEQPOEISORTIVIQQQTIAQHACVNSTELLIQIVAAINAGIPLGNT 120  
 Qy 121 SNOQSHWDLGSSPFAGTVTTIGFONISPRTEGGKFCITYALIPLFGFLAVGVDQ 180  
 Db 121 SNOQSHWDLGSSPFAGTVTTIGFONISPRTEGGKFCITYALIPLFGFLAVGVDQ 180  
 Qy 181 LGTIFGKGIAKYEDTFIKWNVSQTKRISTIILIFGCVLFAVPAIFKIEGSALD 240  
 Db 181 LGTIFGKGIAKYEDTFIKWNVSQTKRISTIILIFGCVLFAVPAIFKIEGSALD 240  
 Qy 241 AIYFVVIITLTIGFDPYAGGSDFIYDLYKTRRLSVEYDKFORATSYRKLSAELGNHQ 360  
 Db 241 AIYFVVIITLTIGFDPYAGGSDFIYDLYKTRRLSVEYDKFORATSYRKLSAELGNHQ 360  
 Qy 301 KKTKEEVGEFRAHAETNTAEEKETTRRLSVEYDKFORATSYRKLSAELGNHQ 360  
 Db 301 KKTKEEVGEFRAHAETNTAEEKETTRRLSVEYDKFORATSYRKLSAELGNHQ 360  
 Qy 361 ELTPCERTLSYNHTSEREVPLPLKAESIYLNGLTPHCAGEDIAVIENTK 411  
 Db 361 ELTPCERTLSYNHTSEREVPLPLKAESIYLNGLTPHCAGEDIAVIENTK 411

US-10-349-528-20  
; Sequence 20, Application US/10349528  
; Publication No. US20040253668A1  
; GENERAL INFORMATION:  
; APPLICANT: RAMANATHAN, Chandra  
; APPLICANT: GOPAL, Shuba  
; APPLICANT: MINTIER, Gabe  
; APPLICANT: FEDER, John  
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR (GPCR) VARIANTS AND METHODS OF  
; USE THEREOF  
; FILE REFERENCE: D0210  
; CURRENT APPLICATION NUMBER: US/10/349,528  
; CURRENT FILING DATE: 2003-01-22  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO: 20  
; LENGTH: 422  
; TYPE: PRT  
; ORGANISM: HOMO SAPIENS  
; US-10-349-528-20

Query Match 97.5%; Score 2038; DB 16; Length 422;

Best Local Similarity 95.9%; Pred. No. 1. 3e-184; Mismatches 13; Indels 0; Gaps 0;

Qy	1	MAAPDLIDPKSAAQNSKPRLSFSKSKPTVLASRVESDSDAINVMKWKTYSTTIFLVVVLVLI 60
Db	12	LAAPDLIDPKSAAQNSKPRLSFSKSKPTVLASRVESDSDAINVMKWKTYSTTIFLVVVLVLI 71
Qy	61	GAAVPKALEQPQEISQRTIVIQQKQTFLAQHACVNSTDELIQIVIAINGIPIGNS 120
Db	72	GATVPKALEQPHEISQRTIVIQQKQTFSQHSCVNSTDELIQIVIAINGIPIGLNT 131
Qy	121	SNOQSHWDLGSSFFAGTVTTIGFGNNSPRTGGKTCITVYALLGFLFGFLLAGYDQ 180
Db	132	SNOQSHWDLGSSFFAGTVTTIGFGNNSPRTGGKTCITVYALLGFLFGFLLAGYDQ 191
Qy	181	LGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFLFGCVLFVALPAVFKHIGWSAID 240
Db	192	LGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFLFGCVLFVALPAVFKHIGWSAID 251
Qy	241	AIVFVVIITLTIGFDYAGGSDEIYDFYKPVWFWLVLGLAYFAAVLSMIGDWLRVIS 300
Db	252	AIVFVVIITLTIGFDYAGGSDEIYDFYKPVWFWLVLGLAYFAAVLSMIGDWLRVIS 311
Qy	301	KCTKEEVGFRAHAETNTAEEKFTRRLSVEIYKFRATSVKRLSABLAGHINO 360
Db	312	KCTKEEVGFRAHAETNTAEEKFTRRLSVEIYKFRATSVKRLSABLAGHINO 371
Qy	361	ELTPCRRTLSVNHLSEREVLPPLKAESIYIYLGLTPHCAGEDIAVENMK 411
Db	372	ELTPCRRTLSVNHLSERDVLPPLKTESIYIYLGLTPHCAGEDIAVENNIK 422

RESULT 10

US-08-816-011-45

; Sequence 45, Application US/08816011  
; Publication No. US20030165806A1

; APPLICANT: Price, Laura A.  
; APPLICANT: Pausch, Mark H.  
; TITLE OF INVENTION: Potassium Channels, Nucleotide Sequences Encoding Them, and Methods of Using Same  
; NUMBER OF SEQUENCES: 56  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: American Home Products Corporation  
; STREET: One Campus Drive  
; CITY: Parsippany  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07054  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

RESULT 11

US-10-870-492-45

; Sequence 45, Application US/10870492  
; Publication No. US2005032165A1  
; GENERAL INFORMATION:  
; APPLICANT: PAUSCH, MARK H.  
; TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,  
; TITLE OF INVENTION: AND METHODS OF USING SAME  
; FILE REFERENCE: 01142-0114 SEQUENCE LISTING  
; CURRENT APPLICATION NUMBER: US/10/870,492  
; CURRENT FILING DATE: 2004-06-18  
; PRIOR APPLICATION NUMBER: US/09/503,849  
; PRIOR FILING DATE: 2000-02-15  
; PRIOR APPLICATION NUMBER: US/816,011  
; PRIOR FILING DATE: 1997-03-11  
; PRIOR APPLICATION NUMBER: PCT/US95/14364  
; PRIOR FILING DATE: 1995-10-25  
; PRIOR APPLICATION NUMBER: 07/332,312

PRIOR FILING DATE: 1994-10-31  
 NUMBER OF SEQ ID NOS: 74  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO: 45  
 LENGTH: 426  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-870-492-45

Query Match Score 96.2%; Score 2011; DB 17; Length 426;  
 Best Local Similarity 95.1%; Pred. No. 5e-182; Indels 0; Gaps 0;  
 Matches 391; Conservative 13; Mismatches 7;

Qy	1 MAAPDILDPKSAAQNSKPRLSFSSKPTVLLASRVEEDSAINVMKWKTIVSTIFLVWLYLII 60	Qy	1 MAAPDILDPKSAAQNSKPRLSFSSKPTVLLASRVEEDSAINVMKWKTIVSTIFLVWLYLII 60
Db	16 VAAPDILDPKSAQNSKPRLSFSTKPTVLLASRVEEDTINMKWKTIVSTIFLVWLYLII 75	Db	16 VAAPDILDPKSAQNSKPRLSFSTKPTVLLASRVEEDTINMKWKTIVSTIFLVWLYLII 75
Qy	61 GAAVFKALEQPEISORTTIVQKOTFIAQHACVNSTELDELIOQIVAAINAGIPLGNS 120	Qy	61 GAAVFKALEQPEISORTTIVQKOTFIAQHACVNSTELDELIOQIVAAINAGIPLGNS 120
Db	76 GATVFKALEQPEHEISORTTIVQKOTFISQHSCVNSTELDELIOQIVAAINAGIPLGNT 135	Db	76 GATVFKALEQPEHEISORTTIVQKOTFISQHSCVNSTELDELIOQIVAAINAGIPLGNT 135
Qy	121 SNOQSHWDLGSSFFAGTVTTIGFGNISPRTEGGKFCIYALGIPLFPLLAVGQDQ 180	Qy	121 SNOQSHWDLGSSFFAGTVTTIGFGNISPRTEGGKFCIYALGIPLFPLLAVGQDQ 180
Db	136 SNOQSHWDLGSSFFAGTVTTIGFGNISPRTEGGKFCIYALGIPLFPLLAVGQDQ 195	Db	136 SNOQSHWDLGSSFFAGTVTTIGFGNISPRTEGGKFCIYALGIPLFPLLAVGQDQ 195
Qy	181 LGTIFGKIAKVEDFIKWNVSQTKIRIISTIIFLFGCVLFVALPAVIFKHIEGSALD 240	Qy	181 LGTIFGKIAKVEDFIKWNVSQTKIRIISTIIFLFGCVLFVALPAVIFKHIEGSALD 240
Db	196 LGTIFGKIAKVEDFIKWNVSQTKIRIISTIIFLFGCVLFVALPAVIFKHIEGSALD 255	Db	196 LGTIFGKIAKVEDFIKWNVSQTKIRIISTIIFLFGCVLFVALPAVIFKHIEGSALD 255
Qy	241 AIFYVVTIITLTIGFDYVAGGSDIEYLDFTYKPVWVNEWLYGLAYPAAVLSMIGDWLRVIS 300	Qy	241 AIFYVVTIITLTIGFDYVAGGSDIEYLDFTYKPVWVNEWLYGLAYPAAVLSMIGDWLRVIS 300
Db	256 KTKKEEVGEFRHAETWTANTAEFKETRRLSVEIYDKFQRATSKRKLSAELGNHQ 360	Db	256 KTKKEEVGEFRHAETWTANTAEFKETRRLSVEIYDKFQRATSKRKLSAELGNHQ 360
Qy	301 KTKKEEVGEFRHAETWTANTAEFKETRRLSVEIYDKFQRATSKRKLSAELGNHQ 375	Qy	301 KTKKEEVGEFRHAETWTANTAEFKETRRLSVEIYDKFQRATSKRKLSAELGNHQ 375
Db	316 KTKKEEVGEFRHAETWTANTAEFKETRRLSVEIYDKFQRATSKRKLSAELGNHQ 375	Db	316 KTKKEEVGEFRHAETWTANTAEFKETRRLSVEIYDKFQRATSKRKLSAELGNHQ 375
Qy	361 ELTPCRTLTSVNLHTSEREVPLPLKTESIYLNGLPHCAGEDIVIENMK 411	Qy	361 ELTPCRTLTSVNLHTSEREVPLPLKTESIYLNGLPHCAGEDIVIENMK 411
Db	376 ELTPCRTLTSVNLHTSEREVPLPLKTESIYLNGLPHCAGEDIVIENMK 426	Db	376 ELTPCRTLTSVNLHTSEREVPLPLKTESIYLNGLPHCAGEDIVIENMK 426
<b>RESULT 13</b> US-10-870-492-58			
; Sequence 58, Application US/10870492			
; Publication No. US2005032165A1			
; GENERAL INFORMATION:			
; APPLICANT: PAUSCH, MARK H.			
; TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,			
; TITLE OF INVENTION: AND METHODS OF USING SAME			
; FILE REFERENCE: 01142_0114			
; CURRENT APPLICATION NUMBER: US/10/870_492			
; CURRENT FILING DATE: 2004-06-18			
; PRIOR APPLICATION NUMBER: US/09/503_849			
; PRIOR FILING DATE: 2000-02-15			
; SEQ ID NO: 58			
; PRIOR APPLICATION NUMBER: PCT/US95/14364			
; PRIOR FILING DATE: 1995-10-25			
; PRIOR APPLICATION NUMBER: 07/332_312			
; PRIOR FILING DATE: 1994-10-31			
; NUMBER OF SEQ ID NOS: 74			
; SOFTWARE: Patent-In Ver. 2.1			
; SEQ ID NO: 58			
; LENGTH: 426			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
; US-10-870-492-58			
Query Match 96.0%; Score 2006; DB 17; Length 426;			
Best Local Similarity 94.9%; Pred. No. 1.5e-181;			
Matches 390; Conservative 14; Mismatches 7; Indels 0; Gaps 0;			
<b>RESULT 14</b> US-10-870-492-57			
; Sequence 57, Application US/10870492			
; Publication No. US2005032165A1			
; GENERAL INFORMATION:			
; APPLICANT: PAUSCH, MARK H.			
; TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,			
; TITLE OF INVENTION: AND METHODS OF USING SAME			
; FILE REFERENCE: 01142_0114			
; CURRENT APPLICATION NUMBER: US/10/870_492			
; CURRENT FILING DATE: 2004-06-18			
; PRIOR APPLICATION NUMBER: US/09/503_849			
; PRIOR FILING DATE: 2000-02-15			
; PRIOR APPLICATION NUMBER: 08/816_011			
; SEQ ID NO: 57			
; LENGTH: 426			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
; US-10-870-492-57			
Query Match 96.0%; Score 2007; DB 17; Length 426;			
Best Local Similarity 94.9%; Pred. No. 1.2e-181;			
Matches 390; Conservative 13; Mismatches 8; Indels 0; Gaps 0;			

RESULT 14		RESULT 15	
Db	196 LGTFGKGAKVEDFTKNNVSQTKIRISTIIFLFGCVLFVALPAIKHIEWSALD 255	Db	376 ELTPCRTLTSVNHLTSERDVLPLKLTESTIYNGLPHCAGEBIAVENIK 426
Qy	241 AIFYVITLTTIGFSDYVAGGSDEIYLDFTKPVWFWILVGLAYPAAVLSMIGDWLRVIS 300	Qy	241 AIFYVITLTTIGFSDYVAGGSDEIYLDFTKPVWFWILVGLAYPAAVLSMIGDWLRVIS 300
Db	256 AIFYVITLTTIGFSDYVAGGSDEIYLDFTKPVWFWILVGLAYPAAVLSMIGDWLRVIS 315	Db	256 AIFYVITLTTIGFSDYVAGGSDEIYLDFTKPVWFWILVGLAYPAAVLSMIGDWLRVIS 315
Qy	301 KKTKEVGFRHAETWANTAEFKETRRLSVEIDKPDWVNLWILVGLAYPAAVLSMIGDWLRVIS 360	Qy	301 KKTKEVGFRHAETWANTAEFKETRRLSVEIDKPDWVNLWILVGLAYPAAVLSMIGDWLRVIS 360
Db	316 KKTKEVGFRHAETWANTAEFKETRRLSVEIDKPDWVNLWILVGLAYPAAVLSMIGDWLRVIS 375	Db	316 KKTKEVGFRHAETWANTAEFKETRRLSVEIDKPDWVNLWILVGLAYPAAVLSMIGDWLRVIS 375
Qy	361 ELTPCRTLTSVNHLTSEREYLPLKAKTSEYNGLPHCAGEBIAVENIK 411	Qy	361 ELTPCRTLTSVNHLTSEREYLPLKAKTSEYNGLPHCAGEBIAVENIK 411
Db	376 ELTPCRTLTSVNHLTSERDVLPLKLTESTIYNGLPHCAGEBIAVENIK 426	Db	376 ELTPCRTLTSVNHLTSERDVLPLKLTESTIYNGLPHCAGEBIAVENIK 426
Query Match Score 60; Application US/10870492			
Publication No. US20050032165A1.			
GENERAL INFORMATION:			
APPLICANT: PAUSCH, MARK H.			
TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM, AND METHODS OF USING SAME			
FILE REFERENCE: 01142-0114 9044 SEQUENCE LISTING			
CURRENT APPLICATION NUMBER: US/10/870,492			
CURRENT FILING DATE: 2004-06-18			
PRIOR APPLICATION NUMBER: US/09/503, 849			
PRIOR FILING DATE: 2000-02-15			
PRIOR APPLICATION NUMBER: US/10/870-492, 60			
PRIOR FILING DATE: 1997-03-11			
SOFTWARE: PatentIn Ver. 2.1			
SEQ ID NO 60			
LENGTH: 426			
TYPE: PRT			
ORGANISM: Homo sapiens			
US-10-870-492-60			
Query Match Score 2003; DB 17; Length 426;			
Best Local Similarity 9.9%; Pred. No. 2.9e-181; Mismatches 8; Indels 0; Gaps 0;			
Matches 390; Conservative 13; Mismatches 8; Indels 0; Gaps 0;			
1 MAAPDLDPKSAAQNSKPRISFSKPKVLAQRVSEDSAINVMKWKTYSTIFLYVLYLII 60			
2 16 VAAPDLDPKSAAQNSKPRISFSKPKVLAQRVSEDSAINVMKWKTYSTIFLYVLYLII 75			
Qy 61 GAAVFKALEQOEISORTTIVIQKOTFIQHACVNSTELDELIQIVAAINAGIPLGNS 120			
Db 76 GATVFKALEQOEISORTTIVIQKOTFIQHACVNSTELDELIQIVAAINAGIPLGNT 135			
Qy 121 SNQSHWDLGSSFFAGTIVTIGFNISPRTEGGKIFCITYALGIPFLFGFLLAGVGDQ 180			
Db 136 SNQSHWDLGSSFFAGTIVTIGFNISPRTEGGKIFCITYALGIPFLFGFLLAGVGDQ 195			
Qy 181 LGTIFGKGIAKVEDFTIKWNVSQTKIRISTIIFTLFGCVLFVLAQVFLKHEGWSALD 240			
Db 196 LGTIFGKGIAKVEDFTIKWNVSQTKIRISTIIFTLFGCVLFVLAQVFLKHEGWSALD 255			
Qy 241 AIFYVITLTTIGFSDYVAGSSDIBLDFYKPVWFMFLVGLAYFAVLSMIGDWLRVIS 300			
Db 256 AIFYVITLTTIGFSDHVGSSDIEYLDFYKPVWFMFLVGLAYFAVLSMIGLVRVIS 315			
Qy 301 KKTKEVGFRHAETWANTAEFKETRRLSVEIDKPDWVNLWILVGLAYPAAVLSMIGDWLRVIS 360			
Db 316 KKTKEVGFRHAETWANTAEFKETRRLSVEIDKPDWVNLWILVGLAYPAAVLSMIGDWLRVIS 375			
Qy 361 ELTPCRTLTSVNHLTSEREYLPLKAKTSEYNGLPHCAGEBIAVENIK 411			
Db 376 ELTPCRTLTSVNHLTSERDVLPLKLTESTIYNGLPHCAGEBIAVENIK 426			
Search completed: July 13, 2005, 09:07:01			
Job time : 91.2442 sec			
RESULT 15			
US-10-870-492-59			
Sequence 59; Application US/10870492			
Publication No. US20050032165A1.			
GENERAL INFORMATION:			
APPLICANT: PAUSCH, MARK H.			
TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM, AND METHODS OF USING SAME			
FILE REFERENCE: 01142-0114 9044 SEQUENCE LISTING			
CURRENT APPLICATION NUMBER: US/10/870,492			
CURRENT FILING DATE: 2004-06-18			
PRIOR APPLICATION NUMBER: US/09/503, 849			
PRIOR FILING DATE: 2000-02-15			
PRIOR APPLICATION NUMBER: US/10/870-492, 60			
SOFTWARE: PatentIn Ver. 2.1			
SEQ ID NO 59			
LENGTH: 426			
TYPE: PRT			
ORGANISM: Homo sapiens			
US-10-870-492-59			
Query Match Score 2003; DB 17; Length 426;			
Best Local Similarity 9.9%; Pred. No. 2.9e-181; Mismatches 8; Indels 0; Gaps 0;			
Matches 390; Conservative 13; Mismatches 8; Indels 0; Gaps 0;			
1 MAAPDLDPKSAAQNSKPRISFSKPKVLAQRVSEDSAINVMKWKTYSTIFLYVLYLII 60			
2 16 VAAPDLDPKSAAQNSKPRISFSKPKVLAQRVSEDSAINVMKWKTYSTIFLYVLYLII 75			
Qy 61 GAAVFKALEQOEISORTTIVIQKOTFIQHACVNSTELDELIQIVAAINAGIPLGNS 120			
Db 76 GATVFKALEQOEISORTTIVIQKOTFIQHACVNSTELDELIQIVAAINAGIPLGNT 135			
Qy 121 SNOQSHWDLGSSFFAGTIVTIGFNISPRTEGGKIFCITYALGIPFLFGFLLAGVGDQ 180			
Db 136 SNOQSHWDLGSSFFAGTIVTIGFNISPRTEGGKIFCITYALGIPFLFGFLLAGVGDQ 195			
Qy 181 LGTFGKGAKVEDFTKNNVSQTKIRISTIIFTLFGCVLFVLAQVFLKHEGWSALD 240			
Db 196 LGTFGKGAKVEDFTKNNVSQTKIRISTIIFTLFGCVLFVLAQVFLKHEGWSALD 255			
Qy 241 AIFYVITLTTIGFSDYVAGSSDIBLDFYKPVWFMFLVGLAYFAVLSMIGDWLRVIS 300			
Db 256 AIFYVITLTTIGFSDYVAGSSDIEYLDFYKPVWFMFLVGLAYFAVLSMIGDWLRVIS 315			
Qy 301 KKTKEVGFRHAETWANTAEFKETRRLSVEIDKPDWVNLWILVGLAYPAAVLSMIGDWLRVIS 360			
Db 316 KKTKEVGFRHAETWANTAEFKETRRLSVEIDKPDWVNLWILVGLAYPAAVLSMIGDWLRVIS 375			
Qy 361 ELTPCRTLTSVNHLTSEREYLPLKAKTSEYNGLPHCAGEBIAVENIK 411			
Db 376 ELTPCRTLTSVNHLTSERDVLPLKLTESTIYNGLPHCAGEBIAVENIK 426			

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OM protein - protein search, using sw model

Run on: July 13, 2005, 08:10:49 ; Search time 26.3635 Seconds  
(without alignments)

1163.760 Million cell updates/sec

Title: US-09-503-089A-4  
Perfect score: 2090  
Sequence: 1 MAAPDLDPKSAAQNSKPRI.....LNGLTPHCAGEDIVIENMK 411

Scoring table: BLOSUM62  
Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:  
 1: /cggn2\_6\_ptodata/1/iaa/5A\_COMB.dep:  
 2: /cggn2\_6\_ptodata/1/iaa/5B\_COMB.dep:  
 3: /cggn2\_6\_ptodata/1/iaa/6A\_COMB.dep:  
 4: /cggn2\_6\_ptodata/1/iaa/6B\_COMB.dep:  
 5: /cggn2\_6\_ptodata/1/iaa/PCT05\_Comb.dep:  
 6: /cggn2\_6\_ptodata/1/iaa/backfile1.dep:  
 \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	2084	99.7	411	3	US-09-236-080-6	Sequence 6, Appli
2	2044	97.8	411	3	US-09-236-080-2	Sequence 2, Appli
3	2044	97.8	411	3	US-09-334-642A-83	Sequence 83, Appli
4	1855	88.8	370	3	US-09-14-914-8	Sequence 8, Appli
5	1251.5	59.9	538	4	US-09-94-016-7001	Sequence 7368, AP
6	1251.5	59.9	558	4	US-09-94-016-7368	Sequence 2, Appli
7	797	38.1	393	4	US-09-432-470-2	Sequence 4, Appli
8	797	38.1	393	4	US-09-432-470-4	Sequence 4, Appli
9	797	38.1	419	4	US-09-94-016-6913	Sequence 6913, AP
10	797	38.1	440	4	US-09-94-016-7809	Sequence 7809, AP
11	551	26.4	107	3	US-09-236-080-4	Sequence 4, Appli
12	420	20.1	499	4	US-09-561-763-2	Sequence 2, Appli
13	420	20.1	499	4	US-09-144-914-2	Sequence 2, Appli
14	392	18.8	361	4	US-09-362-842-14	Sequence 14, Appli
15	387	18.5	332	4	US-09-561-763-5	Sequence 5, Appli
16	387	18.5	332	4	US-09-431-367B-5	Sequence 5, Appli
17	376.5	18.0	336	3	US-09-74-816-2	Sequence 2, Appli
18	376.5	18.0	336	3	US-09-144-914-2	Sequence 2, Appli
19	370	17.7	394	3	US-09-144-914-4	Sequence 4, Appli
20	345.5	16.5	388	4	US-09-94-016-7631	Sequence 7631, AP
21	345	16.5	405	3	US-09-144-914-5	Sequence 5, Appli
22	342	16.4	313	3	US-09-334-643A-81	Sequence 81, Appli
23	342	16.4	313	3	US-09-561-763-8	Sequence 8, Appli
24	342	16.4	313	4	US-09-431-367B-8	Sequence 8, Appli
25	317.5	15.2	408	4	US-09-362-842-12	Sequence 12, Appli
26	299.5	14.3	618	1	US-08-332-312-2	Sequence 2, Appli
27	293	14.0	257	4	US-09-943-016-6654	Sequence 6654, AP

## ALIGNMENTS

RESULT 1									
US-09-236-080-6									
; Sequence 6, Application US/09236080									
; Patent No. 6242217									
; GENERAL INFORMATION:									
; APPLICANT: Conrad Chapman									
; TITLE OF INVENTION: No. 6242217el Compounds									
; FILE REFERENCE: GP20031									
; CURRENT APPLICATION NUMBER: US/09/236, 080									
; CURRENT FILING DATE: 1999-01-25									
; NUMBER OF SEQ ID NOS: 6									
; SOFTWARE: FastSEQ for Windows Version 3.0									
; SEQ ID NO: 6									
; LENGTH: 411									
; TYPE: PRT									
; ORGANISM: Mus musculus									
; US-09-236-080-6									
Query	Match	99.7%	Score	2084;	DB 3;	Length	411;		
Best Local Similarity	99.8%	Pred.	No.	1.9e-210;					
Matches	410;	Conservative	1;	Mismatches	0;	Gaps	0;		

**RESULT 2**  
 US-09-236-080-2  
 Sequence 2, Application US/09236080  
 Patent No. 6242217  
 GENERAL INFORMATION:  
 APPLICANT: Helen Meadows  
 TITLE OF INVENTION: No. 6242217el Compounds  
 FILE REFERENCE: GP30031  
 CURRENT APPLICATION NUMBER: US/09/236, 080  
 CURRENT FILING DATE: 1999-01-15  
 NUMBER OF SEQ ID NOS: 6  
 SEQ ID NO 2  
 LENGTH: 411  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-236-080-2

Query Match 97.8%; Score 2044; DB 3; Length 411;  
 Best Local Similarity 96.4%; Pred. No. 3e-206;  
 Matches 396; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MAAPDLDIPKSAQAQSNSKRLSFSSSKPTVLASRVEDSDAINVMKWTSTFLVVVLYLII 60  
 Db 1 MAAPDLDIPKSAQAQSNSKRPLSFSSSKPTVLASRVEDDTINVMKWTSTFLVVVLYLII 60

Qy 61 GAAVFKALEQPEISORTTIVQKOTPIAQHACVNSTELDELQIVAAINAGIPLGNS 120  
 Db 61 GATVFKALEQPEISORTTIVQKOTPIAQHACVNSTELDELQIVAAINAGIPLGNT 120

Qy 121 SNOQSHWDLGSSFFAGTVTTIGCGNISPTEGGKIFCITYALGIPLEGFLLAGVGQDQ 180  
 Db 121 SNOQSHWDLGSSFFAGTVTTIGCGNISPTEGGKIFCITYALGIPLEGFLLAGVGQDQ 180

Qy 181 LGTIGKGIAKVEDPIKWNVSQTKRIISTIPLFGCVLFVAPAVIKHGEGWSALD 240  
 Db 181 LGTIGKGIAKVEDPIKWNVSQTKRIISTIPLFGCVLFVAPAVIKHGEGWSALD 240

Qy 241 AYFVVTILTTIGFDYVAGGSDFIYLDFYKPVWFWLVLGLAYFAAVLSMIGDWLRVIS 300  
 Db 241 AYFVVTILTTIGFDYVAGGSDFIYLDFYKPVWFWLVLGLAYFAAVLSMIGDWLRVIS 300

Qy 301 KKTKEEVGEFRAAETWANTAEFKETRRLSVEYDKEORATSVKRKLSAELAGHNQ 360  
 Db 301 KKTKEEVGEFRAAETWANTAEFKETRRLSVEYDKEORATSVKRKLSAELAGHNQ 360

Qy 361 ELTPCRTLTSVNLTSERVLPLKKAESTIYNGLTPHCAGEDIAVIENMK 411  
 Db 361 ELTPCRTLTSVNLTSERVLPLKKAESTIYNGLTPHCAGEDIAVIENTK 411

RESULT 4  
 US-09-144-914-8  
 Sequence 8, Application US/09144914  
 Patent No. 6309855  
 GENERAL INFORMATION:  
 APPLICANT: Duprat, Fabrice  
 APPLICANT: Lesage, Florian  
 APPLICANT: Pink, Michel  
 APPLICANT: Lazdunski, Michel  
 APPLICANT: Current Application Number: US/09/144,914  
 CURRENT FILING DATE: 1998-09-01  
 EARLIER APPLICATION NUMBER: 08/749,816  
 EARLIER FILING DATE: 1996-11-15  
 EARLIER APPLICATION NUMBER: 60/095,234  
 EARLIER FILING DATE: 1998-08-04  
 EARLIER APPLICATION NUMBER: FR 96/01565  
 EARLIER FILING DATE: 1996-02-08  
 NUMBER OF SEQ ID NOS: 24  
 SOFTWARE: Patentin Ver. 2.0  
 SEQ ID NO 8  
 LENGTH: 370  
 TYPE: PRT  
 ORGANISM: Murine  
 FEATURE:  
 OTHER INFORMATION: TREK-1  
 US-09-144-914-8

Query Match 88.8%; Score 1855; DB 3; Length 370;

**RESULT 3**  
 US-09-336-643A-83  
 Sequence 83, Application US/09336643A  
 Patent No. 6399761  
 GENERAL INFORMATION:  
 APPLICANT: Miller, Andrew P.  
 APPLICANT: Curran, Mark Edward  
 APPLICANT: Hu, Ping  
 APPLICANT: Rutter, Marc  
 APPLICANT: Wang, Jian-Wang  
 TITLE OF INVENTION: Human Potassium Channels  
 FILE REFERENCE: SEQ-15P  
 CURRENT APPLICATION NUMBER: US/09/336,643A  
 CURRENT FILING DATE: 1999-06-18  
 PRIOR APPLICATION NUMBER: 60/1076,687  
 PRIOR FILING DATE: 1998-08-07  
 PRIOR APPLICATION NUMBER: 60/116,448  
 PRIOR FILING DATE: 1999-01-19  
 PRIOR APPLICATION NUMBER: PCT/US99/03826

*No one third w/  
no one third w/  
or plus.*

Best Local Similarity 99.5%; Pred. No. 2e-186; Matches 366; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MAAPDLDPSAQAONSKPRLSSSPTVLASRVEDSDAINVMKRTVSTIFLVVLYLII 60  
Db 1 MAAPDLDPSAQAONSKPRLSSSPTVLASRVEDSDAINVMKRTVSTIFLVVLYLII 60  
QY 61 GAAVPKALBOPQEISORTTIVIQQTKFIAHQACVNSTELDELIQIVAAINAGITPLNS 120  
Db 61 GAAVPKALBOPQEISORTTIVIQQTKFIAHQACVNSTELDELIQIVAAINAGITPLNS 120  
QY 121 SNOQSHWDLGSSPFPAQTIVTTGGNISPRTEGGKFCITVALLGIPFLLAGVGDQ 180  
Db 121 SNOQSHWDLGSSPFPAQTIVTTGGNISPRTEGGKFCITVALLGIPFLLAGVGDQ 180  
QY 181 LGTFGKGIAKVEDFIKNNVSQTKIRIISTIIFLGCVLFVLPATVFKHTEGWSALD 240  
Db 181 LGTFGKGIAKVEDFIKNNVSQTKIRIISTIIFLGCVLFVLPATVFKHTEGWSALD 240  
QY 241 AIVPVVITTTTGGDYVAGGSDEIYLDKPKVNMFWILVGLAYFAAVLSMIGDWLRVIS 300  
Db 241 AIVPVVITTTTGGDYVAGGSDEIYLDKPKVNMFWILVGLAYFAAVLSMIGDWLRVIS 300  
QY 301 KKTKEEVGEFRHAETWANTTAEKFETRRLSVYEIDKFORATSVKLSSAELAGNINQ 360  
Db 301 KKTKEEVGEFRHAETWANTTAEKFETRRLSVYEIDKFORATSVKLSSAELAGNINQ 360  
QY 361 ELTPCRRRT 368  
Db 361 ELTPCRRRT 368

RESULT 5  
US-09-949-016-7001  
; Sequence '7001', Application US/09949016  
; Patent No. 681239  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949, 016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241, 755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237, 768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231, 498  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO: 7368  
; LENGTH: 558  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-7368  
Query Match 59.9%; Score 1251.5; DB 4; Length 558;  
Best Local Similarity 64.3%; Prod. No. 1.1e-122; Mismatches 54; Indels 17; Gaps 5;  
Matches 247; Conservative 54; N mismatches 66; In dels 17; Gaps 5;

QY 2 AAPDLDPKSA-----AQNSKPLRSFSKPKTVLASRVE SDS--AINVMKMKTVSTI 50  
Db 17 AAAPVCPQPKSATNGGPPAPPTPLRSSRATVVA-RMEGTSQGGLOTVMKMTVVAI 75  
QY 51 FLVVVLYLIGAAYVKALEQPKQSQRITIVIQQTKFIAHQACVNSTELDLIQIVAI 110  
Db 76 FVVVVVLYLIGVFLAREQPKFESSQNTIALAEFLRDHVCVSPQEBETLJQHALDAD 135  
QY 111 NAGTIPLENSSNOVSHWDLGSSFFAGTIVTTGGNISPRTEGGKFCITVALLGIPFL 170  
Db 136 NAGTIPLENSSNOVSHWDLGSSFFAGTIVTTGGNISPRTEGGKFCITVALLGIPFL 195  
QY 171 GPLLAGVGDDQLGTFGKGIAKVEDFIKNNVSQTKIRIISTIIFLGCVLFVLPATVFKHTEGWSALD 230  
Db 196 GPLLAGVGDDQLGTFGKGIAKVEDFIKNNVSQTKIRIISTIIFLGCVLFVLPATVFKHTEGWSALD 255  
QY 231 KHIEGWSALDAIIFVVVITTTGFDYVAGG-SDEIYLDKPKVNMFWILVGLAYFAAVL 289  
Db 276 KYIEGWTALLESIYFVVVLTGFDYVAGGAGNINREWYRPLWFMVILVGLAYFAAVL 335  
QY 290 SMIGDWLRVISKTKTEEKEFRHAETWANTTAEKFETRRLSVYEIDKFORATSV-- 346  
Db 336 SMIGDWLRVISKTKTEEKEFRHAETWANTTAEKFETRRLSVYEIDKFORATSV-- 395  
QY 347 -KRLSAELAGNNQELTPCRRTL 369  
Db 396 ERRRLGIDQRAHSIDMLSPERKS 419



RESULT 10

US-99-949-016-7809 Sequence 7809 Application US/09949016

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLO01307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

SEQ ID NO: 7809

SOFTWARE: FastSEQ for Windows Version 4.0

TYPE: PRT

ORGANISM: Human

US-09-949-016-7809

	Matches	107	Conservative	0	Mismatches	0	Indels	0	Gaps	0
Qy	119	NSSNQYSHWDLGSSPFPEAGTYTTTGFGNNSPRTEGGKIFCITYALGIPLFGFYLAGVG	178							
Db	1	NSSNQYSHWDLGSSPFPEAGTYTTTGFGNNSPRTEGGKIFCITYALGIPLFGFYLAGVG	60							

RESULT 12

US-03-561-763-2

Sequence 2, Application US/09561763

Patent No. 666433

GENERAL INFORMATION:

APPLICANT: Curris, Rory A.J. et al.

TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR

FILE REFERENCE: MNI-074CP2

CURRENT APPLICATION NUMBER: US/09/561,763

PRIOR APPLICATION NUMBER: 09/431,367

PRIOR FILING DATE: 2000-04-29

PRIOR APPLICATION NUMBER: 09/431,367

PRIOR FILING DATE: 01-11-1999

PRIOR FILING DATE: 01-03-1999

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 2

LENGTH: 499

TYPE: PRT

ORGANISM: Homo sapiens

US-09-561-763-2

	Matches	102	Conservative	0	Mismatches	0	Indels	0	Gaps	0
Qy	42	MWKVTVSTPLWLYLIGRAVKALEQPOEISQRTTIVQKOTFIAGHACVNTELDE	101							
Db	48	MRSTLLAALVLVNLVSGALVFALEQPHQDQEGBVREKFLRHPCVSQELGL	107							
Qy	102	LIQQIAAAINAGIPLGNSSNQVS- -WLGSSPFPEAGTYTTTGFGNNSPRTEGGKIFC	159							
Db	108	LIKEVADALGGGADPETSNSNSHSANDLSAPPSTGTTTGYNTVALRTDAGLRC	167							
Qy	160	LIYALGIPLFGLAGVQQLGTLFGKGAKVDTFIKWNVSQPKIRLISTIFILFGC	219							
Db	166	IPYAVGIPFGLLQGVDRLGSSLRHGICHLVPLHVPBELLVRVSPAMFILLG	227							
Qy	220	VLFVALPAVIFKHIEGWWSALDAYVITLTTTIGFGDYVAGGS DIEYLFLYKPVVWFML	279							
Db	228	LLFLVLTPTVFCMDWSKLEAYVIVITLTTVFGDYVAGADPRODSPAYQPLVWFML	287							
Qy	280	VGLAYFAVISMIGWLRVLSKTKKEEVGFRAHAEWTANVA	323							
Db	288	LGLAYFASTLTTGWLWVYSRTRAEMLGSLTAQASWGTGVTY	331							

RESULT 11

US-09-236-080-4

Sequence 4, Application US/09236080

Patent No. 6242217

GENERAL INFORMATION:

APPLICANT: Helen Meadows

APPLICANT: Conrad Chapman

TITLE OF INVENTION: No. 6242217el Compounds

FILE REFERENCE: GP30031

CURRENT APPLICATION NUMBER: US/09/236,080

CURRENT FILING DATE: 1999-01-25

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 4

LENGTH: 107

TYPE: PRT

ORGANISM: Homo sapiens

US-09-236-080-4

	Matches	551	Conservative	0	Mismatches	0	Indels	0	Gaps	0
Qy	119	NSSNQYSHWDLGSSPFPEAGTYTTTGFGNNSPRTEGGKIFCITYALGIPLFGFYLAGVG	178							
Db	1	NSSNQYSHWDLGSSPFPEAGTYTTTGFGNNSPRTEGGKIFCITYALGIPLFGFYLAGVG	60							

RESULT 13

US-09-431-367B-2

Sequence 2, Application US/09431367B

Patent No. 6670149

GENERAL INFORMATION:

APPLICANT: Curis, Rory A.J.

TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR

FILE REFERENCE: MNI-074CP

CURRENT APPLICATION NUMBER: US/09/431,367B

CURRENT FILING DATE: 1999-01-01

PRIOR FILING DATE: 1999-03-01  
 NUMBER OF SEQ ID NOS: 12  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 2 LENGTH: 499  
 TYPE: PRT ORGANISM: Homo sapiens  
 US-09-431-367B-2

Query Match Score 20.1%; Best Local Similarity 30.8%; Matches 105; Conservative 62; Mismatches 120; Indels 54; Gaps 11; Length 499;

Qy 54 VVLYLIGAAVFKALEQPQEISORTTIVIQTKTIAQHACVNSTELDELIQVIAINAG 113  
 Db 12 IIFYLIGAAFEVLEPHWKEAKNYYTQLHLIKEPCLGQEGIDKLEVSDAAGG 71

Qy 114 IPIGLNSSNQVSHWDLGSSPFAGATVITIGFGNTSPRTGGKLFCTIYALLGIPFGL 173  
 Db 72 VAITGNQT - FNNNNWPNAFMIAATVITIGGYGNVAPKTAGRLFCVFLGFVPL--C 126

Qy 174 LAGVGDLQGTIFGKGIAKVEDPTIKNVSQTKIRIISTIFILEGCULFTALPAVFKHI 233  
 Db 127 LTWI-SALGKFFGGRAKRLGOFLTTRGVSURKAQITCTVTFIVNGSVLWVIPPFVEMVT 185

Qy 234 EGWNSALDAVYIIPVITLTTIQRGDDYVA-GSDIEYLDYFKEVWWFMILVGLAYFAVLSNI 292  
 Db 186 EGWNVIIBGLYTSFITISTIGDFTAGVNPISANTHALYRFVELMVLGLAW---LSLP 241

Qy 293 GDWLRLVISKKTKEEYGBFRHAEAENTANTAEAEKETRRLSVELYDKFQRATSVKRKLSA 352  
 Db 242 VNW-----KVSMF-----VEVHAKIKRRRR-----RKESF 267

Qy 353 BLAGNINQELTPCRRTLSVNLTSREV - LPPLIKAESTY 391  
 Db 268 E-SSPHS-----RKAHQKGSTASKDNVNFSLSKKETRY 301

RESULT 14 US-09-362-842-14  
 Sequence 14, Application US/09362842  
 Patent No. 6511824  
 GENERAL INFORMATION:  
 APPLICANT: Buchman et al.  
 TITLE OF INVENTION: NUCLEAR ACIDS AND POLYPEPTIDES OF INVERTEBRATE TWIK  
 CHANNELS AND METHODS OF USE  
 FILE REFERENCE: 7326-104  
 CURRENT APPLICATION NUMBER: US/09/362,842  
 CURRENT FILING DATE: 1999-07-28  
 PRIOR APPLICATION NUMBER: 09/270,767  
 NUMBER OF SEQ ID NOS: 70  
 SEQ ID NO 14  
 LENGTH: 361  
 ORGANISM: Leptinotarsa decemlineata  
 US-09-362-842-14

Query Match Score 18.8%; Best Local Similarity 35.6%; Matches 89; Conservative 53; Mismatches 86; Indels 22; Gaps 6; Length 361;

Qy 56 LYLIIGAAVFKALEQPQEISORTTIVIQTKTIAQHACVNSTELDELIQVIAINAGII 115  
 Db 55 MFLCSGAAVSYFEABERLRVKGATAVOKPLVFNPNNTDADLEBLIVTRANNRGVS 114

Qy 116 PLGNSNQVSHWDLGSSPFAGATVITIGFGNTSPRTGGKLFCTIYALLGIPFGL 175  
 Db 115 AENATSE-PWSFGGSFFFASVTTTIGGHVTPLSRNGKLFCMFYAVVGIPLTLVLLS 173

Qy 176 GVGDQL-GTIFGKGIAKVEDPTIKNVSQ-----TKRIISTIIFTLFGCVLFVALP 226

Db 174 ALVERILLIPTVW-----LIQWLNLSKLGHLYQPLRIRVHLAIIVVLLVFLLLP 223  
 Qy 227 AVIFKHIE-GWSALDAVYIIPVITLTTIGFGDYVAGGSDE-YLDFYKPVWFWILVGLAY 284  
 Db 224 AAIPASLBEWDYIUDSLYYCFISLTIGGDYIPGDSAHQPYRPLYKMTTCYLFGLTI 283  
 Qy 285 FAAVLSMIGD  
 Db 284 MMILITVYD 293

RESULT 15 US-09-561-763-5  
 Sequence 5, Application US/09561763  
 Patent No. 6664313  
 GENERAL INFORMATION:  
 APPLICANT: Curris, Rory A.J. et al.  
 TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR  
 FILE REFERENCE: MN1-074CP2  
 CURRENT APPLICATION NUMBER: US/09/561,763  
 CURRENT FILING DATE: 2000-04-29  
 PRIOR APPLICATION NUMBER: 09/431,367  
 PRIOR FILING DATE: 01-11-1999  
 PRIOR APPLICATION NUMBER: US 09/259,951  
 PRIOR FILING DATE: 01-03-1999  
 NUMBER OF SEQ ID NOS: 12  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 5  
 LENGTH: 332;  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-561-763-5

Query Match Score 18.5%; Best Local Similarity 35.5%; Matches 88; Conservative 51; Mismatches 95; Indels 14; Gaps 6;

Qy 50 IFLVVVYLIGAAVFKALEQPQEISORTTIVIQTKTIAQHACVNSTELDELIQVVA 109  
 Db 25 LLLAYLAYLAAGTGVWTFLEGRAAQDSSRSFQNDKWEILQNFCLDRPALSIRDVVQA 84

Qy 110 INAGITIPLGNSSNQVSHWDLGSSPFAGATVITIGFGNTSPRTGGKIFCITYALGIPL 169  
 Db 85 YRNGLSLLNTS-MGRWLVGSFFSVSTITIGYGNLSPNTMAARLFCIFFALVGPIL 143

Qy 170 FGFLLAGVDPDOLGTIFGKGCI----AKVETTFTKVNVSQPKIRIISTIIFLGCVLFVAL 225  
 Db 144 NLVYVIL---NRIGHIMOOGVNHWA,SRLGCT---WQ-DPDKARWLGASGAILSGLLFLLL 195

Qy 226 PAVIFKHIEGWSALDAVYIIPVITLTTIGFGDYVAGGSDE-YLDFYKPVWFWILVGLAY 284  
 Db 196 PPLIFSHMEGSWSVTTGFFAFITLSTVGFSDYVGMNPSQRYPLWYKOMVSLWTFGMNW 255

Qy 285 FAAVLSMI 292  
 Db 256 LALIKLI 263

Search completed: July 13, 2005, 08:47:05  
 Job time : 27.3635 secs

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OM protein - protein search, using sw model.

Run on: July 13, 2005, 07:58:54 ; Search time 101.398 Seconds  
(without alignments)

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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3:	geneseqp20008:*
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8:	geneseqp20048:*

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26 1243 59.2 543 7 ADE08315 Novel pro  
27 1243 59.2 543 8 ADN62910 Human NOV  
28 1239 59.0 543 5 AAU79473 Human nov  
29 1215.5 57.9 724 5 AAQ14193 Human tri  
30 988 47.0 228 8 ADJ27190 Human TRI  
31 803 38.2 392 6 ABU50891 Human G P  
32 803 38.2 393 3 AAY94426 Human h-T  
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38 803 38.2 419 8 ADH51639 Human TWI  
39 803 38.2 419 8 ADI27936 Human TWI  
40 803 38.2 419 8 ADR4894 Polypepti  
41 803 38.2 1314 4 AAU04571 Human G-P  
42 780.2 38.2 1314 6 ABU60872 Human G P  
43 776.5 37.0 398 2 AAV30647 A mechani  
44 768.5 36.6 398 5 AAE16598 Human TWI  
45 636 30.3 383 4 ABG02731 Novel hum

## ALIGNMENTS

RESULT 1  
AAE10341

ID AAE10341 standard; protein: 411 AA.

XX

AC AAE10341;

XX

DT 10-DEC-2001 (first entry)

XX

DE Human TREK-1 potassium channel protein.

XX

KW Human; potassium channel protein; TREK-1; anaesthetic; analgesia;  
anesthesia.

XX

OS Homo sapiens.

XX

PN WO2000047738-A2.

XX

PD 17-AUG-2000.

XX

PP 11-FEB-2000; 2000WO-1B000226.

XX

PR 12-FEB-1999; 99US-0119727P.

PR 11-FEB-2000; 2000US-00503089.

XX

PA (CNRS ) CNRS CENT NAT RECH SCI.

XX

PI Lazdunski M, Honore E, Lesage F, Romey G, Patel AJ;

XX

DR 2000-549146/50.

DR N-FSDB; AAD17496.

XX

PT Novel nucleic acid encoding a TREK-1 potassium channel protein for  
transfecting cells to be used to identify compounds with anaesthetic  
properties.

XX

CC The invention relates to human and mouse TREK-1 potassium channel  
proteins and their corresponding DNA molecules. TREK-1 nucleic acid is  
useful for transfecting cells to induce expression of the TREK-1  
potassium channel protein. These cells are then used in assays to  
identify compounds which have anaesthetic properties, producing a safe,  
reversible state of unconsciousness with concurrent amnesia and analgesia,  
in a mammal upon inhalation. The present sequence is human TREK-1

CC potassium channel protein

XX Sequence 411 AA;

SQ

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query	Match Length	DB ID	Description
1	A10341	3	AAE10341	Aaa10341 Human TRE
2	Aaa10341	3	Aaa10341	Aaa10341 Human pot
3	Aaa10341	3	Aaa10341	Aaa10341 Human h-TREK1 P
4	Aaa10341	3	Aaa10341	Aaa10341 Human TRE
5	Aaa10341	3	Aaa10341	Aaa10341 Human GPC
6	Aaa10341	3	Aaa10341	Aaa10341 Human two
7	Aaa10341	3	Aaa10341	Aaa10341 Human TWI
8	Aaa10341	3	Aaa10341	Aaa10341 Human GPC
9	Aaa10341	3	Aaa10341	Aaa10341 Human pot
10	Aaa10341	3	Aaa10341	Aaa10341 Human pot
11	Aaa10341	3	Aaa10341	Aaa10341 Human pot
12	Aaa10341	3	Aaa10341	Aaa10341 Human pot
13	Aaa10341	3	Aaa10341	Aaa10341 Human pot
14	Aaa10341	3	Aaa10341	Aaa10341 Murine TR
15	Aaa10341	3	Aaa10341	Aaa10341 Mouse h-T
16	Aaa10341	3	Aaa10341	Aaa10341 Human
17	Aaa10341	3	Aaa10341	Aaa10341 Human DIR
18	Aaa10341	3	Aaa10341	Aaa10341 Human TRE
19	Aaa10341	3	Aaa10341	Aaa10341 Human h-T
20	Aaa10341	3	Aaa10341	Aaa10341 Human pol
21	Aaa10341	3	Aaa10341	Aaa10341 Human TR
22	Aaa10341	3	Aaa10341	Aaa10341 Novel hum
23	Aaa10341	3	Aaa10341	Aaa10341 Human nov
24	Aaa10341	3	Aaa10341	Aaa10341 Hypothala
25	Aaa10341	3	Aaa10341	Aaa10341 Novel NOV

Query Match	100.0%	Score 2100; DB 3;	Length 411;	
Best Local Similarity	100.0%	Pred. No. 8	8e-20;	
Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1	MAADLLDPKSAAGNSKPRLSFSTKPTVLASRVEDSTTINWKWTKYSTTIFLYVVLILLI	60	
Db	1	MAADLLDPKSAAGNSKPRLSFSTKPTVLASRVEDSTTINWKWTKYSTTIFLYVVLILLI	60	
QY	61	GATYKALEQPHETISORTTIVIQKOTFSQHSCVNSTDELQIQAIAINGIIPGNT	120	
Db	61	GATYKALEQPHETISORTTIVIQKOTFSQHSCVNSTDELQIQAIAINGIIPGNT	120	
QY	121	SNOISWHDLGSSPPFAGVITIGFGNSSPTEGGKTCIYTALGFLFGFLLAGYGDQ	180	
Db	121	SNOISWHDLGSSPPFAGVITIGFGNSSPTEGGKTCIYTALGFLFGFLLAGYGDQ	180	
QY	181	LGTIFGKGAKVDTFIKWNVSQTKIRISTIIFTILFCVLFVALPATIKHIEGWSALD	240	
Db	181	LGTIFGKGAKVDTFIKWNVSQTKIRISTIIFTILFCVLFVALPATIKHIEGWSALD	240	
QY	241	AIVFVITLTTIGFGDYAGGSDEIYLIFYKPVWFMVFLVGLAYFAAVLSMIGDWLRVIS	300	
Db	241	AIVFVITLTTIGFGDYAGGSDEIYLIFYKPVWFMVFLVGLAYFAAVLSMIGDWLRVIS	300	
QY	301	KKTKKEBEVGFRAHAETWANTVAFKETPRLSVEIYDKFQRTSIKRLKSAELAGHNQ	360	
Db	301	KKTKKEBEVGFRAHAETWANTVAFKETPRLSVEIYDKFQRTSIKRLKSAELAGHNQ	360	
QY	361	ELTPCRRTLSVNHLTNERDVLPPLKTESIYLGLPFCAGEIAVENIK	411	
Db	361	ELTPCRRTLSVNHLTNERDVLPPLKTESIYLGLPFCAGEIAVENIK	411	
RESULT 2				
ID AAY34133				
XX standard; protein; 411 AA.				
AC AAY34133;				
XX DT 30-NOV-1999 (first entry)				
XX DE Human potassium channel K+Hnovo59.				
XX KW Potassium channel; ataxia; arrhythmia; epilepsy; Bartter's syndrome; cardiovascular disorder; CNS disorder; renal disorder.				
OS Homo sapiens.				
XX PN WO9943696-A1.				
XX PD 02-SEP-1999.				
XX PF 22-FEB-1999; 93WO-US003826.				
XX PR 25-FEB-1998; 98US-0076682P.				
PR 07-AUG-1998; 98US-0095833P.				
PR 19-JAN-1999; 98US-0116444P.				
XX PA (AXYS-) AXYS PHARM INC.				
XX PI Miller AP, Curran ME, Hu P, Rutter M, Wang J;				
XX WPI: 1999-527591/44.				
DR N-PSDB; AAZ1915.				
XX PR New nucleic acids encoding mammalian K+Hnovo potassium channel proteins, useful for the diagnosis and treatment of episodic ataxia with myokymia, cardiac arrhythmia, epilepsy and Bartter's syndrome.				
XX PS Claim 3; Page 104-105; 112pp; English.				
XX CC This sequence represents the human K+Hnovo59 potassium channel. K+Hnovo proteins have a high degree of homology to known potassium channels and				
CC may be alpha subunits, which form the functional channel, or accessory subunits that act to modulate the channel activity. K+Hnovo59 is a 4 transmembrane domain, 2 pore domain potassium channel. The gene is located on chromosome 19, determined via PCR chromosomal localisation using primers ARZ11939 and AAZ11940. K+Hnovo cDNAs were isolated by extension of expressed sequence tags (ESTs) which were related but not identical to known human potassium channels. Potential polymorphisms detected as sequence variants between multiple independent clones.				
CC Potassium channels have critical roles in various cell types and biochemical pathways. Defective potassium channels are known to cause four human diseases: episodic ataxia with myokymia; cardiac arrhythmia (long QT syndrome); epilepsy and Bartter's syndrome. As potassium channels are critical components of virtually all cells, it is likely that abnormal potassium channels are also implicated in certain renal, cardiovascular and central nervous system (CNS) disorders. Nucleotides encoding K+Hnovo proteins may be used for identifying homologous or related proteins and the DNA sequences encoding them. They may be used to produce compositions that modulate the expression and function of the K+Hnovo protein and in studying the biochemical pathways associated with it. They may also be used for the recombinant production of K+Hnovo protein in fermentation cultures. Additionally, such nucleotides may be used in gene therapy protocols for the treatment of diseases associated with abnormal potassium channels.				
Sequence 411 AA:				
Query Match	99.8%	Score 2095; DB 2;	Length 411;	
Best Local Similarity	99.8%	Pred. No. 2.9e-209;		
Matches 410; Conservative 1; Mismatches 0; Indels 0; Gaps 0;				
Qy 1 MAAPDLDPKSAAGNSKPRLSFSTKPTVLARVESDTTINWKWTKYSTTFLVWVLYLII	60			
Db 1 MAAPDLDPKSAAGNSKPRLSFSTKPTVLARVESDTTINWKWTKYSTTFLVWVLYLII	60			
Qy 1 MAAPDLDPKSAAGNSKPRLSFSTKPTVLARVESDTTINWKWTKYSTTFLVWVLYLII	60			
Db 1 MAAPDLDPKSAAGNSKPRLSFSTKPTVLARVESDTTINWKWTKYSTTFLVWVLYLII	60			
Qy 61 GATVFKALEQPHETISORTTIVQKOTFSQHSCVNSTDELQIQAIAINGIIPGNT	120			
Db 61 GATVFKALEQPHETISORTTIVQKOTFSQHSCVNSTDELQIQAIAINGIIPGNT	120			
Qy 121 SNOISWHDLGSSPPFAGVITIGFGNSSPTEGGKTCIYTALGFLFGFLLAGYGDQ	180			
Db 121 SNOISWHDLGSSPPFAGVITIGFGNSSPTEGGKTCIYTALGFLFGFLLAGYGDQ	180			
Qy 181 LGTIFGKGAKVDTFIKWNVSQTKIRISTIIFTILFCVLFVALPATIKHIEGWSALD	240			
Db 181 LGTIFGKGAKVDTFIKWNVSQTKIRISTIIFTILFCVLFVALPATIKHIEGWSALD	240			
Qy 241 AIVFVITLTTIGFGDYAGGSDEIYLIFYKPVWFMVFLVGLAYFAAVLSMIGDWLRVIS	300			
Db 241 AIVFVITLTTIGFGDYAGGSDEIYLIFYKPVWFMVFLVGLAYFAAVLSMIGDWLRVIS	300			
Qy 301 KKTKKEBEVGFRAHAETWANTVAFKETPRLSVEIYDKFQRTSIKRLKSAELAGHNQ	360			
Db 301 KKTKKEBEVGFRAHAETWANTVAFKETPRLSVEIYDKFQRTSIKRLKSAELAGHNQ	360			
Qy 361 ELTPCRRTLSVNHLTNERDVLPPLKTESIYLGLPFCAGEIAVENIK	411			
Db 361 ELTPCRRTLSVNHLTNERDVLPPLKTESIYLGLPFCAGEIAVENIK	411			
RESULT 3				
ID AAY28496				
XX standard; protein; 411 AA.				
AC AAY28496;				
XX DT 12-OCT-1999 (first entry)				
XX DE h-TREK1 polypeptide.				
XX KW h-TREK1; two pore potassium channel; inflammatory disease;				
XX CC chromosome 1q32.				
OS Homo sapiens.				

XX XX 19-MAR-2001 (first entry)  
 PN XX DE Human TREK.  
 PD XX KW Human; TREK; 2P domain potassium channel; resting membrane potential;  
 XX KW neuronal excitability; neurotransmitter release modulation; epilepsy;  
 PF 02-DEC-1998; 98WO-EP007805.  
 PR 27-JAN-1998; 98EP-00300570.  
 PR 09-OCT-1998; 98GB-00022135.  
 PA (SMITHKLINE BEECHAM PLC.)  
 XX Homo sapiens  
 PT Meadow HJ, Chapman CG;  
 XX PN WO00072863-A2.  
 DR XX 07-DEC-2000.  
 XX PD 01-JUN-2000; 2000WO-GB002107.  
 PT XX 01-JUN-1999; 99GB-00012733.  
 XX (SMITHKLINE BEECHAM PLC.)  
 CC PA Hervieu GJ, Meadows HJ, Randall AD;  
 CC XX DR 2001-080422/09.  
 CC XX N-PSDB; AAC0412.  
 CC XX Use of human TREK1 polypeptide, polynucleotides encoding them and  
 CC PT modulators of h-TREK1 polypeptides for treating epilepsy, sleep-related  
 CC PT disorders, addiction and dyskinetias including Parkinson's and Huntington's  
 CC PT chorea.  
 XX PS Claim 7; Page 29; 35pp; English.  
 XX CC The present sequence is human TREK1 (h-TREK1). h-TREK1 is a member of the  
 CC 2P domain potassium channel family of proteins which play a part in the  
 CC control of resting membrane potential. Modulation of these channels will  
 CC therefore affect neuronal excitability, thereby leading to a modulation  
 CC of neurotransmitter release and activity of neuronal networks. Such  
 CC modulation therefore may be useful for the treatment of certain  
 CC neurological conditions such as epilepsy, sleep-related disorders,  
 CC cognitive dysfunction, attention deficit disorder, addiction,  
 CC anxiety/phobia, Parkinson's and Huntington's chorea, cerebral palsy,  
 CC incontinence, erectile dysfunction or alopecia.  
 XX SQ Sequence 411 AA;  
 Query Match 99.8%; Score 2095; DB 2; Length 411;  
 Best Local Similarity 99.8%; Pred. No. 2.9e-209;  
 Matches 410; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MAADLLDIDPKSAQNSKPLRSFSTKPTVLSRVEDTINVMWKRTVSTIFLYVVLII 60  
 Db 1 MAADLLDIDPKSAQNSKPLRSFSTKPTVLSRVEDTINVMWKRTVSTIFLYVVLII 60  
 Qy 61 GATVFKALQPHETSRQTTIVQKQTFSQHSCVNSTELIQQIVAAINAGIPIGLNT 120  
 Db 61 GATVFKALQPHETSRQTTIVQKQTFSQHSCVNSTELIQQIVAAINAGIPIGLNT 120  
 Qy 121 SNOQSHWDLGSSPFAGTVITIGFNIISPRTEGGKICITIYALLGIPFGFLLAGYDQ 180  
 Db 121 SNOQSHWDLGSSPFAGTVITIGFNIISPRTEGGKICITIYALLGIPFGFLLAGYDQ 180  
 Qy 181 LGTFGKGIAKVEDTFLKVNVSQTKIRIISTIIFLFCVLFALPATIFKHEGMSLD 240  
 Db 181 LGTFGKGIAKVEDTFLKVNVSQTKIRIISTIIFLFCVLFALPATIFKHEGMSLD 240  
 Qy 241 AYFVVIITTCGFDYAGGSDEIYDFYKPVWFMILVGLAYFAAVLSMIGDMLRVIS 300  
 Db 241 AYFVVIITTCGFDYAGGSDEIYDFYKPVWFMILVGLAYFAAVLSMIGDMLRVIS 300  
 Qy 301 KCKTKEEVGEFRAAEAETVNTAEEFKETRRRLSVEIYKFKQRTASIKKLSAELAGHNQ 360  
 Db 301 KCKTKEEVGEFRAAEAETVNTAEEFKETRRRLSVEIYKFKQRTASIKKLSAELAGHNQ 360  
 Qy 361 ELTPCRRTLSVNHLTNEBDVLPPLKTSIYLTPHCAGEIAVENIK 411  
 Db 361 ELTPCRRTLSVNHLTSEBDVLPPLKTSIYLTPHCAGEIAVENIK 411  
 Qy 411 LGTFGKGIAKVEDTFLKVNQSQTKIRIISTIIFLFCVLFALPATIFKHEGMSLD 240  
 Db 411 LGTFGKGIAKVEDTFLKVNQSQTKIRIISTIIFLFCVLFALPATIFKHEGMSLD 240  
 Qy 241 AYFVVIITTCGFDYAGGSDEIYDFYKPVWFMILVGLAYFAAVLSMIGDMLRVIS 300  
 Db 241 AYFVVIITTCGFDYAGGSDEIYDFYKPVWFMILVGLAYFAAVLSMIGDMLRVIS 300  
 AC 241 AYFVVIITTCGFDYAGGSDEIYDFYKPVWFMILVGLAYFAAVLSMIGDMLRVIS 300

RESULT 4  
 AB50044 Standard; protein: 411 AA.  
 ID AB50044  
 XX AB50044  
 AC AB50044



-1. In rats, TREK-1 is highly expressed in much of the brain and is inhibited by protein kinase C and protein kinase C mediated phosphorylation. It is activated by volatile general anesthetics and is expressed at high levels in the brain of sleep animals. Based on these criteria and on experimental results, it is hypothesized that TREK-1 is a key mediator of sleep (when open) and waking (when closed). The invention provides methods for identifying a sleep- or wakefulness-promoting compound based on the compound's ability to modulate two pore domains in K<sup>+</sup> channels such as TREK-1. It also provides screening methods for isolating short sleep, no rebound and sleep deprivation resistant Drosophila mutants useful for identifying sleep-related molecular targets.

XX

SQ

Sequence 411 AA;

Query Match 99.8%; Score 2095; DB 8; Length 411;

Best Local Similarity 99.8%; Pred. No. 2.9e-209;

Matches 410; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db

Qy 1 MAADLLDPKSAQNSKPRISFSTKPTVLASRVEDDTINVMKRTVSTIFLYVVLVLI 60

Db 1 MAADLLDPKSAQNSKPRISFSTKPTVLASRVEDDTINVMKRTVSTIFLYVVLVLI 60

Qy 61 GATVPKALQPHETISQRTTIVIQKOTFISQHSCYNSTDELQQIVAAINAGITPLGNT 120

Db 61 GATVPKALQPHETISQRTTIVIQKOTFISQHSCYNSTDELQQIVAAINAGITPLGNT 120

Qy 121 SNOQSHWDLGSSFFPAGTVTTFGNNSPRTEGGKIFCITYALLGIPLFGLLAGYSDQ 180

Db 121 SNOQSHWDLGSSFFPAGTVTTFGNNSPRTEGGKIFCITYALLGIPLFGLLAGYSDQ 180

Qy 181 LGTIFGKGIAKVEDFIKVNVSQPKIRIISTIIFLGCVLFTVALPAIKHIEGWSALD 240

Db 181 LGTIFGKGIAKVEDFIKVNVSQPKIRIISTIIFLGCVLFTVALPAIKHIEGWSALD 240

Qy 241 AYFVVTIITLGDFDYAGGSDEIYLDKPYVWFLVGLAYFAAVLSMIGDWLRVIS 300

Db 241 AYFVVTIITLGDFDYAGGSDEIYLDKPYVWFLVGLAYFAAVLSMIGDWLRVIS 300

Qy 301 KCTKEEVGFRAAEWTANVTAFFKEFERRLSVEIYDFQRATSIEKLSAELAGNINQ 360

Db 301 KCTKEEVGFRAAEWTANVTAFFKEFERRLSVEIYDFQRATSIEKLSAELAGNINQ 360

Qy 361 ELTPCRRTLSVNHLTNERDVLPLKTKTSIYLNGLTPHCAGEETAVINIK 411

Db 361 ELTPCRRTLSVNHLTNERDVLPLKTKTSIYLNGLTPHCAGEETAVINIK 411

Qy 7

Db AAE16597

Qy AAE16597 standard; protein; 411 AA.

Db AAE16597;

Qy 18-APR-2002 (First entry)

Db Human TWIK-Related K<sup>+</sup> Channel-1 (TREK-1) protein.Qy Human; TWIK-Related K<sup>+</sup> Channel-1; TREK-1; anaesthetic; screening.

Db Homo sapiens.

Qy Key Location/Qualifiers

Db Key Region 47..65

Qy Note= "M1 membrane spanning segment"

Db Domain 127..150

Qy Note= "P1 pore domain"

Db Region 158..178

Qy Note= "M2 membrane spanning segment"

Db Region 209..230

Qy Note= "M3 membrane spanning segment"

Db Domain 236..259

Qy Note= "P2 pore domain"

Db Region 274..293

Qy Result 8

Db ADP03575 standard; protein; 422 AA.

/note= "M4 membrane spanning segment"  
 FT XX WO200200715-A2.

CC PN 03-JAN-2002.

CC PD 27-JUN-2001; 2001WO-1B001436.

CC PF 27-JUN-2000; 2000US-0214559P.

CC PR 27-JUN-2001; 2001US-00892360.

CC PA (CNRS ) CNRS CENT NAT RECH SCI.

XX PI Lazdunski M, Lescage F, Romeo G;

XX DR WPI; 2002-139903/18.

XX New mammalian K<sup>+</sup> channel protein with two pore domains, for screening various compounds, particularly for identifying biologically active compounds with anaesthetic properties.

XX Disclosure: Fig 1A; Sopp: English.  
 PS

XX The invention relates to a mammalian K<sup>+</sup> channel protein with two pore domains, called TREK2 (TWIK-Related K<sup>+</sup> Channel). The protein produces currents whose current-voltage relationship is slightly inwardly rectifying in high symmetrical K<sup>+</sup> conditions. TREK2 is a member of the fatty acid sensitive K<sup>+</sup> channel family. TREK-2 genes located on chromosome 14q31 is abundantly expressed in kidney, pancreas and moderately in testis, brain, colon and small intestine. The mammalian K<sup>+</sup> channel protein is useful in methods for screening various compounds. In particular, the protein is useful in methods for identifying biologically active compounds with anaesthetic properties. The present sequence is TREK-1 protein used in the invention

XX SQ Sequence 411 AA;

Query Match 99.6%; Score 2092; DB 5; Length 411;  
 Best Local Similarity 99.8%; Pred. No. 6e-209; Mismatches 1; Indels 0; Gaps 0;

XX Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAAPDLDPKSAQNSKPRISFSTKPTVLASRVEDDTINVMKRTVSTIFLYVVLVLI 60  
 Db 1 MAAPDLDPKSAQNSKPRISFSTKPTVLASRVEDDTINVMKRTVSTIFLYVVLVLI 60

Qy 61 GATVPKALQPHETISQRTTIVIQKOTFISQHSCYNSTDELQQIVAAINAGITPLGNT 120  
 Db 61 GATVPKALQPHETISQRTTIVIQKOTFISQHSCYNSTDELQQIVAAINAGITPLGNT 120

Qy 121 SNOQSHWDLGSSFFPAGTVTTFGNNSPRTEGGKIFCITYALLGIPLFGLLAGYSDQ 180  
 Db 121 SNOQSHWDLGSSFFPAGTVTTFGNNSPRTEGGKIFCITYALLGIPLFGLLAGYSDQ 180

Qy 181 LGTIFGKGIAKVEDFIKVNVSQPKIRIISTIIFLGCVLFTVALPAIKHIEGWSALD 240  
 Db 181 LGTIFGKGIAKVEDFIKVNVSQPKIRIISTIIFLGCVLFTVALPAIKHIEGWSALD 240

Qy 241 AYFVVTIITLGDFDYAGGSDEIYLDKPYVWFLVGLAYFAAVLSMIGDWLRVIS 300  
 Db 241 AYFVVTIITLGDFDYAGGSDEIYLDKPYVWFLVGLAYFAAVLSMIGDWLRVIS 300

Qy 301 KCTKEEVGFRAAEWTANVTAFFKEFERRLSVEIYDFQRATSIEKLSAELAGNINQ 360  
 Db 301 KCTKEEVGFRAAEWTANVTAFFKEFERRLSVEIYDFQRATSIEKLSAELAGNINQ 360

Qy 361 ELTPCRRTLSVNHLTNERDVLPLKTKTSIYLNGLTPHCAGEETAVINIK 411  
 Db 361 ELTPCRRTLSVNHLTNERDVLPLKTKTSIYLNGLTPHCAGEETAVINIK 411

Qy 7  
 Db AAE16597

Qy AAE16597 standard; protein; 411 AA.

Db AAE16597;

Qy 18-APR-2002 (First entry)

Db Human TWIK-Related K<sup>+</sup> Channel-1 (TREK-1) protein.

Qy Human; TWIK-Related K<sup>+</sup> Channel-1; TREK-1; anaesthetic; screening.

Db Homo sapiens.

Qy Key Location/Qualifiers

Db Key Region 47..65

Qy Note= "M1 membrane spanning segment"

Db Domain 127..150

Qy Note= "P1 pore domain"

Db Region 158..178

Qy Note= "M2 membrane spanning segment"

Db Region 209..230

Qy Note= "M3 membrane spanning segment"

Db Domain 236..259

Qy Note= "P2 pore domain"

Db Region 274..293

XX SQ Result 7

XX ID AAE16597

XX Qy AAE16597 standard; protein; 411 AA.

XX Db AAE16597;

XX Qy 18-APR-2002 (First entry)

XX Db Human TWIK-Related K<sup>+</sup> Channel-1 (TREK-1) protein.

XX Qy Human; TWIK-Related K<sup>+</sup> Channel-1; TREK-1; anaesthetic; screening.

XX Db Homo sapiens.

XX Qy Key Location/Qualifiers

XX Db Key Region 47..65

XX Qy Note= "M1 membrane spanning segment"

XX Db Domain 127..150

XX Qy Note= "P1 pore domain"

XX Db Region 158..178

XX Qy Note= "M2 membrane spanning segment"

XX Db Region 209..230

XX Qy Note= "M3 membrane spanning segment"

XX Db Domain 236..259

XX Qy Note= "P2 pore domain"

XX Db Region 274..293

XX Qy Result 8

XX ID ADP03575

XX Qy ADP03575 standard; protein; 422 AA.



SQ	Sequence 426 AA;	Query Match Score 98.2%; Best Local Similarity 98.5%; Matches 405; Conservative Matches 405; Mismatches 3; Indels 0; Gaps 0;	Length 426;
Qy	1 MAAPDLIDPKSAQNSKPLRSFSTKPTYLASRVEDDTINMKWTKTYSITIFLVVVLII 60		
Db	16 VAAPDLIDPKSAQNSKPLRSFSTKPTYLASRVEDDTINMKWTKTYSITIFLVVVLII 75		
Qy	61 GATVFKALEQPHETISQRTTIVIQKQTFSQHSCVNSTELDELQQIYVAINAGIIPGNT 120		
Db	76 GATVFKALEQPHETISQRTTIVIQKQTFSQHSCVNSTELDELQQIYVAINAGIIPGNT 135		
Qy	121 SNOISHWMDLGSSPFPAQGTTITFGNNSPRTGGKICITIYALLGLPFLGFLLAGYDQ 180	XX	Claim 37; Page 113-115; 131pp; English.
Db	136 SNOISHWMDLGSSPFPAQGTTITFGNNSPRTGGKICITIYALLGLPFLGFLLAGYDQ 195	XX	The invention relates to a mutant potassium ion channel protein, having four membrane spanning domains and two pore forming domains, comprising a mutation at the second pore forming domain. The expression of the mutant protein in a cell confers improved inward potassium flux and the ability to grow in the presence of potassium. Mutant proteins and their corresponding polynucleotide sequences can therefore be used to improve inward potassium flux into cells under acidic conditions by modulating the membrane potential using therapeutic agents. The sequences may be used to develop agonists and antagonists of potassium channel proteins in order to control pests such as nematodes and insects. This sequence represents a human transmembrane potassium ion channel TPKC1 mutant protein
SQ	Sequence 426 AA;	Query Match Score 98.0%; Best Local Similarity 98.3%; Matches 404; Conservative Matches 404; Mismatches 3; Indels 0; Gaps 0;	Length 426;
Qy	1 MAAPDLIDPKSAQNSKPLRSFSTKPTYLASRVEDDTINMKWTKTYSITIFLVVVLII 60	1	MAAPDLIDPKSAQNSKPLRSFSTKPTYLASRVEDDTINMKWTKTYSITIFLVVVLII 60
Db	16 VAAPDLIDPKSAQNSKPLRSFSTKPTYLASRVEDDTINMKWTKTYSITIFLVVVLII 75	16	VAAPDLIDPKSAQNSKPLRSFSTKPTYLASRVEDDTINMKWTKTYSITIFLVVVLII 75
Qy	61 GATVFKALEQPHETISQRTTIVIQKQTFSQHSCVNSTELDELQQIYVAINAGIIPGNT 120	61	GATVFKALEQPHETISQRTTIVIQKQTFSQHSCVNSTELDELQQIYVAINAGIIPGNT 120
Db	76 GATVFKALEQPHETISQRTTIVIQKQTFSQHSCVNSTELDELQQIYVAINAGIIPGNT 135	76	GATVFKALEQPHETISQRTTIVIQKQTFSQHSCVNSTELDELQQIYVAINAGIIPGNT 135
Qy	121 SNOISHWMDLGSSPFPAQGTTITFGNNSPRTGGKICITIYALLGLPFLGFLLAGYDQ 180	121	SNOISHWMDLGSSPFPAQGTTITFGNNSPRTGGKICITIYALLGLPFLGFLLAGYDQ 180
Db	136 SNOISHWMDLGSSPFPAQGTTITFGNNSPRTGGKICITIYALLGLPFLGFLLAGYDQ 195	136	SNOISHWMDLGSSPFPAQGTTITFGNNSPRTGGKICITIYALLGLPFLGFLLAGYDQ 195
Qy	181 LGTFIGKIAKYEDTFFIKWNSQTKRKLSTIFLGCVLPLAIFIKGTEGWSALD 240	181	LGTFIGKIAKYEDTFFIKWNSQTKRKLSTIFLGCVLPLAIFIKGTEGWSALD 240
Db	196 LGTFIGKIAKYEDTFFIKWNSQTKRKLSTIFLGCVLPLAIFIKGTEGWSALD 255	196	LGTFIGKIAKYEDTFFIKWNSQTKRKLSTIFLGCVLPLAIFIKGTEGWSALD 255
Qy	241 AIFYVVITLTIGFDYAGGSDEIYLDFYKPVWFMNLVGLAYFAAVLSMIGDWLRVIS 300	241	AIFYVVITLTIGFDYAGGSDEIYLDFYKPVWFMNLVGLAYFAAVLSMIGDWLRVIS 300
Db	256 AIFYVVITLTIGFDYAGGSDEIYLDFYKPVWFMNLVGLAYFAAVLSMIGDWLRVIS 315	256	AIFYVVITLTIGFDYAGGSDEIYLDFYKPVWFMNLVGLAYFAAVLSMIGDWLRVIS 315
Qy	301 KTKTKEEVSEFRAAEWTANVTAFFKETRRRLSVEITKXKFORATSIKKLSAELAGHNQ 360	301	KTKTKEEVSEFRAAEWTANVTAFFKETRRRLSVEITKXKFORATSIKKLSAELAGHNQ 360
Db	316 ELTPCCRRTLSVNHLTNERDVLPLKTESIYNGLPHCAGERIAVENIK 411	316	ELTPCCRRTLSVNHLTNERDVLPLKTESIYNGLPHCAGERIAVENIK 411
Qy	361 ELTPCCRRTLSVNHLTNERDVLPLKTESIYNGLPHCAGERIAVENIK 426	361	ELTPCCRRTLSVNHLTNERDVLPLKTESIYNGLPHCAGERIAVENIK 426
Db	376 ELTPCCRRTLSVNHLTNERDVLPLKTESIYNGLPHCAGERIAVENIK 426	376	ELTPCCRRTLSVNHLTNERDVLPLKTESIYNGLPHCAGERIAVENIK 426
RESULT 10			RESULT 11
AAU07622	AAU07622 standard; protein: 426 AA.	AAU07623	AAU07623 standard; protein: 426 AA.
AC	AAU07622;	AC	AAU07623;
DT	21-NOV-2001 (first entry)	DT	21-NOV-2001 (first entry)
XX	Human potassium ion channel TPKC1 mutant protein #1.	XX	Human potassium ion channel TPKC1 mutant protein #2.
XX	transmembrane potassium ion channel protein; inward potassium flux; pest control; membrane potential; pepticide; antihelminthic; nematode; insect; TPKC1; human; mutant; mutein; mutein.	XX	transmembrane potassium ion channel protein; inward potassium flux; pest control; membrane potential; pepticide; antihelminthic; nematode; insect; TPKC1; human; mutant; mutein.
OS	Homo sapiens.	OS	Homo sapiens.
XX	Key Location/Qualifiers	XX	Key Location/Qualifiers
PH	Misc-difference 256	PH	Misc-difference 272
FT	/note= "Wild-type Ala replaced by Thr"	FT	/note= "Wild-type Tyr replaced by His"
XX		XX	
PN	W0200161006-A2.	PN	W0200161006-A2.
XX	PD 23-AUG-2001.	XX	PD 23-AUG-2001.
XX	PP 14-FEB-2001; 2001WO-US004660.	XX	PP 14-FEB-2001; 2001WO-US004660.
PR	15-FEB-2000; 2000US-00503849.	PR	15-FEB-2000; 2000US-00503849.
XX	(BADI ) BASF CORP.	XX	(BADI ) BASF CORP.
XX	Pausch MH;	XX	Pausch MH;
XX	WPI: 2001-516570/59.	XX	WPI: 2001-516570/59.
DR	N-PSDB; AAS12181.	DR	N-PSDB; AAS12181.
PT	New polypeptide, a mutant potassium ion channel protein for improving inward potassium flux under acidic conditions.	PT	New polypeptide, a mutant potassium ion channel protein for improving inward potassium flux under acidic conditions.
XX		XX	

XX DE Human potassium ion channel TPKC1 mutant protein #4.  
 PP XX  
 XX XX  
 XX KW Transmembrane potassium ion channel protein; inward potassium flux;  
 PR KW pest control; membrane potential; pesticide; antihelmintic; nematode;  
 XX KW insect; TPKC1; human; mutant; mutain.  
 PA XX  
 XX OS Homo sapiens.  
 PI XX  
 Pausch MH;  
 XX FH Key  
 DR FT Misc-difference 270 /note: "Wild-type Gly replaced by Arg"  
 N-PSDB; AAS12180.  
 XX FT  
 PT PN WO200161006-A2.  
 PT XX  
 XX PD 23-AUG-2001.  
 PS XX  
 XX FF 14-FBB-2001; 2001WO-US004680.  
 CC XX  
 CC PR 15-FBB-2000; 2000US-00503849.  
 CC PA (BADI ) BASF CORP.  
 CC PAusach MH;  
 CC PI  
 CC DR WPI; 2001-536570/59.  
 CC N-PSDB; AAS12184.  
 CC XX  
 CC PT New polypeptide, a mutant potassium ion channel protein for improving  
 CC inward potassium flux under acidic conditions.  
 CC XX  
 CC PS Claim 37; Page 115-117; 131pp; English.  
 CC XX  
 CC The invention relates to a mutant potassium ion channel protein, having a  
 CC four membrane spanning domains and two pore forming domains, comprising a  
 CC mutation at the second pore forming domain. The expression of the mutant  
 CC protein in a cell confers improved inward potassium flux and the ability  
 CC to grow in the presence of potassium. Mutant proteins and their  
 CC corresponding polynucleotide sequences can therefore be used to improve  
 CC inward potassium flux into cells under acidic conditions by modulating  
 CC the membrane potential using therapeutic agents. The sequences may be  
 CC used to develop agonists and antagonists of potassium channel proteins in  
 CC order to control pests such as nematodes and insects. This sequence  
 CC represents a human transmembrane potassium ion channel TPKC1 mutant  
 CC protein.  
 XX SQ Sequence 426 AA;  
 Query Match 98.0%; Score 2057; DB 4; Length 426;  
 Best Local Similarity 98.3%; Pred. No. 2.8e-205;  
 Matches 404; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
 Qy 1 MAAPDILDPKSAAQNSKPLRSPTSKPPTLASRVEDDTINWKRKVSTFLVVVLYII 60  
 Db 16 VAPDILDPKSAQNSKPLRSPTSKPPTLASRVEDDTINWKRKVSTFLVVVLYII 75  
 Qy 61 GATVFKAQEHPISORTTIVIQLQKPTPSQHSCVNSTELDILQIQVAAANAGIIPLGN 120  
 Db 76 GATVFKAQEHPISORTTIVIQLQKPTPSQHSCVNSTELDILQIQVAAANAGIIPLGN 135  
 Qy 121 SNQISHNDLGSSPFFACTVTTIGFGNISPRTEGGK1FCLITYALGIPLFGLLAGVGDQ 180  
 Db 136 SNQISHNDLGSSPFFACTVTTIGFGNISPRTEGGK1FCLITYALGIPLFGLLAGVGDQ 195  
 Qy 181 LGTIFGRGIAKVEDTFIKWNVSOTKIRIISTIIFLGCVLFVALPAIFKHEGMSALD 240  
 Db 196 LGTIFGRGIAKVEDTFIKWNVSOTKIRIISTIIFLGCVLFVALPAIFKHEGMSALD 255  
 Qy 241 AIYFVVTIITIGFGDVIAGGSDEIYLDFYKPVVWFLVILGVAYFAVLVSLMIGDWLRVIS 300  
 Db 256 AIYFVVTIITIGFGDVIAGGSDEIYLDFYKPVVWFLVILGVAYFAVLVSLMIGRLVRVIS 315  
 Qy 301 KCTKEEYGEFRHAAFENTANATAEFKTRRLSVEIYDKFQATSKRKLSAELAGNHQ 360  
 Db 316 KCTKEEYGEFRHAAFENTANATAEFKTRRLSVEIYDKFQATSKRKLSAELAGNHQ 375  
 Qy 361 ELTPPCRRLSVNLFTNEBDLPLPLKTESIYNGLTPHCAGEBAIENIK 411  
 Db 376 ELTPPCRRLSVNLFTNEBDLPLPLKTESIYNGLTPHCAGEBAIENIK 426  
 Qy 427 IGTIFGRGIAKVEDTFIKWNVSOTKIRIISTIIFLGCVLFVALPAIFKHEGMSALD 240  
 Db 432 IGTIFGRGIAKVEDTFIKWNVSOTKIRIISTIIFLGCVLFVALPAIFKHEGMSALD 255  
 RESULT 12  
 AUU07645 ID AUU07625 standard; protein: 426 AA.  
 AC XX  
 AC AC  
 XX XX  
 DT NOV-2001 (first entry) XX



Best Local Similarity 96.1%; Pred. No. 1.3e-203; Matches 395; Conservative 12; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MAAPDLDPKSAAQNSKPRLSSTKPTVLASRVEDTTINMKWKTSTIPLVWYLI 60  
Db 1 MAAPDLDPKSAAQNSKPRLSSTKPTVLASRVEDTTINMKWKTSTIPLVWYLI 60

Qy 61 GATVFKRALQEPRHEISQTIVIQKOTRISQHCVNSTELLIQIVAINAGIIPGLNT 120  
Db 61 GAVFKALEQPKQESQRTTIVQKQFIAQHCVNSTELLIQIVAINAGIIPGLNT 120

Qy 121 SNOISHMDLGSSFFFAGSTVITIGFGNISPRTEGGKIFCITYALIGIPLFGFLLAGVGDQ 180  
Db 121 SNOISHMDLGSSFFFAGSTVITIGFGNISPRTEGGKIFCITYALIGIPLFGFLLAGVGDQ 180

Qy 181 LGTIFGKGIAKVEDTFKWNYSQTQKTRIISTIPLFGCULFVALPAIFKHIEGWSALD 240  
Db 181 LGTIFGKGIAKVEDTFKWNYSQTQKTRIISTIPLFGCULFVALPAIFKHIEGWSALD 240

Qy 241 AIVFVITLTTIGFGDYVAGGSDEIYDFYKPVVWWFWILVGLAYFAAVLSMIGDWLRVIS 300  
Db 241 AIVFVITLTTIGFGDYVAGGSDEIYDFYKPVVWWFWILVGLAYFAAVLSMIGDWLRVIS 300

Qy 301 KKTKEEYGEFRHAAEWTANTYTAEFKTRRLSVEIYDKFORATSIKRKLSAELAGNHQ 360  
Db 301 KKTKEEYGEFRHAAEWTANTYTAEFKTRRLSVEIYDKFORATSIKRKLSAELAGNHQ 360

Qy 361 ELTPCRRTLSVNHLTNERDVLPLLTKTSEVYLNGLTPHCAGEDIAVENIK 411  
Db 361 ELTPCRRTLSVNHLTSEREVLPPLKXESIYLNGLTPHCAGEDIAVENIK 411

## RESULT 15

AY28497 standard; protein; 411 AA.

AC AAY28497;

XX DT 12-OCT-1999 (first entry)

DB Mouse h-TREK1 polypeptide.

KW h-TREK1; two pore potassium channel; inflammatory disease;  
chromosome 1q32.  
XX OS Mus musculus.

XX PN WO9937762-A1.

XX PD 29-JUL-1999.

XX PF 02-DEC-1998; 98WO-EP007805.

XX PR 27-JAN-1998; 98EP-00300570.

PR 09-OCT-1998; 98GB-00022135.

XX PA (SMIK ) SMITHKLINE BEECHAM PLC.  
XX PT New two pore potassium channel used for, e.g. treatment of cancer,  
pulmonary, cardiovascular and inflammatory diseases.  
XX Claim 3; Page 26; 44pp; English.

PS WPI; 1999-469126/39.

DR N-PSDB; AA200040.

XX PT This sequence is the mouse h-TREK1 polypeptide, encoded by the h-TREK1  
CC polynucleotide AA200040. h-TREK1 is a two pore potassium channel. The  
CC polynucleotide sequence of h-TREK1 can be used to diagnose a disease or  
CC susceptibility to a disease related to expression or activity of h-TREK-1  
CC polypeptides. The methods of diagnosis may be used in the treatment of

CC diseases including cancer, pulmonary, cardiovascular, and inflammatory  
CC diseases, pain, psychiatric disorders including depression and  
CC schizophrenia, neurodegenerative diseases including Alzheimer's, stroke,  
CC and head trauma and neurological disorders including migraine  
XX SQ Sequence 411 AA;

	Query Match	Score 2035; DB 2;	Length 411;
Best Local Similarity	96.9%;	Score 2035;	Length 411;
Matches	394;	Best Local Similarity	95.9%;
Conservative	12;	Matches	394;
Mismatches	5;	Conservative	12;
Indels	0;	Mismatches	5;
Gaps	0;	Indels	0;
SQ	1 MAAPDLDPKSAAQNSKPRLSSTKPTVLASRVEDTTINMKWKTSTIPLVWYLI 60	1 MAAPDLDPKSAAQNSKPRLSSTKPTVLASRVEDTTINMKWKTSTIPLVWYLI 60	1 MAAPDLDPKSAAQNSKPRLSSTKPTVLASRVEDTTINMKWKTSTIPLVWYLI 60
Db	1 MAAPDLDPKSAAQNSKPRLSSTKPTVLASRVEDTTINMKWKTSTIPLVWYLI 60	1 MAAPDLDPKSAAQNSKPRLSSTKPTVLASRVEDTTINMKWKTSTIPLVWYLI 60	1 MAAPDLDPKSAAQNSKPRLSSTKPTVLASRVEDTTINMKWKTSTIPLVWYLI 60
Qy	61 GATVFKRALQEPRHEISQTIVIQKOTRISQHCVNSTELLIQIVAINAGIIPGLNT 120	61 GATVFKALEQPKQESQRTTIVQKQFISQHSCUNSTELLIQIVAAAGIIPGLNT 120	61 GATVFKALEQPKQESQRTTIVQKQFISQHSCUNSTELLIQIVAAAGIIPGLNT 120
Db	61 GATVFKALEQPKQESQRTTIVQKQFISQHSCUNSTELLIQIVAAAGIIPGLNT 120	61 GATVFKALEQPKQESQRTTIVQKQFISQHSCUNSTELLIQIVAAAGIIPGLNT 120	61 GATVFKALEQPKQESQRTTIVQKQFISQHSCUNSTELLIQIVAAAGIIPGLNT 120
Qy	121 SNOISHMDLGSSFFFAGSTVITIGFGNISPRTEGGKIFCITYALIGIPLFGFLLAGVGDQ 180	121 SNOISHMDLGSSFFFAGSTVITIGFGNISPRTEGGKIFCITYALIGIPLFGFLLAGVGDQ 180	121 SNOISHMDLGSSFFFAGSTVITIGFGNISPRTEGGKIFCITYALIGIPLFGFLLAGVGDQ 180
Db	121 SNOISHMDLGSSFFFAGSTVITIGFGNISPRTEGGKIFCITYALIGIPLFGFLLAGVGDQ 180	121 SNOISHMDLGSSFFFAGSTVITIGFGNISPRTEGGKIFCITYALIGIPLFGFLLAGVGDQ 180	121 SNOISHMDLGSSFFFAGSTVITIGFGNISPRTEGGKIFCITYALIGIPLFGFLLAGVGDQ 180
Qy	181 LGTIFGKGIAKVEDTFKWNYSQTQKTRIISTIPLFGCULFVALPAIFKHIEGWSALD 240	181 LGTIFGKGIAKVEDTFKWNYSQTQKTRIISTIPLFGCULFVALPAIFKHIEGWSALD 240	181 LGTIFGKGIAKVEDTFKWNYSQTQKTRIISTIPLFGCULFVALPAIFKHIEGWSALD 240
Db	181 LGTIFGKGIAKVEDTFKWNYSQTQKTRIISTIPLFGCULFVALPAIFKHIEGWSALD 240	181 LGTIFGKGIAKVEDTFKWNYSQTQKTRIISTIPLFGCULFVALPAIFKHIEGWSALD 240	181 LGTIFGKGIAKVEDTFKWNYSQTQKTRIISTIPLFGCULFVALPAIFKHIEGWSALD 240
Qy	241 AIVFVITLTTIGFGDYVAGGSDEIYDFYKPVVWWFWILVGLAYFAAVLSMIGDWLRVIS 300	241 AIVFVITLTTIGFGDYVAGGSDEIYDFYKPVVWWFWILVGLAYFAAVLSMIGDWLRVIS 300	241 AIVFVITLTTIGFGDYVAGGSDEIYDFYKPVVWWFWILVGLAYFAAVLSMIGDWLRVIS 300
Db	241 AIVFVITLTTIGFGDYVAGGSDEIYDFYKPVVWWFWILVGLAYFAAVLSMIGDWLRVIS 300	241 AIVFVITLTTIGFGDYVAGGSDEIYDFYKPVVWWFWILVGLAYFAAVLSMIGDWLRVIS 300	241 AIVFVITLTTIGFGDYVAGGSDEIYDFYKPVVWWFWILVGLAYFAAVLSMIGDWLRVIS 300
Qy	301 KKTKEEYGEFRHAAEWTANTYTAEFKTRRLSVEIYDKFORATSIKRKLSAELAGNHQ 360	301 KKTKEEYGEFRHAAEWTANTYTAEFKTRRLSVEIYDKFORATSIKRKLSAELAGNHQ 360	301 KKTKEEYGEFRHAAEWTANTYTAEFKTRRLSVEIYDKFORATSIKRKLSAELAGNHQ 360
Db	301 KKTKEEYGEFRHAAEWTANTYTAEFKTRRLSVEIYDKFORATSIKRKLSAELAGNHQ 360	301 KKTKEEYGEFRHAAEWTANTYTAEFKTRRLSVEIYDKFORATSIKRKLSAELAGNHQ 360	301 KKTKEEYGEFRHAAEWTANTYTAEFKTRRLSVEIYDKFORATSIKRKLSAELAGNHQ 360

Search completed: July 13, 2005, 08:39:46  
Job time : 105.398 secs

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OM protein - protein search, using SW model

Run on: July 13, 2005, 08:01:55 ; Search time 93.9622 Seconds  
(without alignments)

2239.886 Million cell updates/sec

Title: US-09-503-089A-2

Perfect score: 2100

Sequence: 1 MAAPDLDPKSAQNSKPRL.....LNGLTPHCAQEIAVIENIK 411

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03:  
1: uniprot\_sprot:  
2: uniprot\_trembl:  
\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2095	99.8	411	2 Q9NRT2	Q9NRT2 homo sapien
2	2079	99.0	411	2 CIW2_HUMAN	Q8HY88 bos taurus
3	2062	98.2	426	1 O6PFB9	O9069 homo sapien
4	2042	97.2	414	2 CIW2_MOUSE	O6PFB9 mus musculus
5	2041	97.2	411	1 Q92056	P97438 mus musculus
6	2025	96.4	426	2 Q92056	Q92056 rattus norvegicus
7	1254	59.7	538	2 O6Q834	O6Q834 oryctolagus cuniculus
8	1250	59.5	453	2 Q8BZB0	Q8BZB0 m muis musculus
9	1249.5	59.5	535	2 Q8BWU1	Q8BWU1 m mus musculus
10	1249	59.5	538	1 CIWA_RAT	Q9184 rattus norvegicus
11	1243	59.2	538	1 CIWA_HUMAN	P57789 homo sapien
12	1243	59.2	543	2 Q6B014	Q6B014 homo sapien
13	1217.5	58.0	546	2 Q6BEY1	O6BEY1 xenopus laevis
14	803	38.2	393	1 CIW4_HUMAN	Q9W98 homo sapien
15	776.5	37.0	398	1 CIW4_MOUSE	O8I454 mus musculus
16	764.5	36.4	397	2 O92414	Q92414 rattus norvegicus
17	616	29.3	241	2 Q9CX88	Q9CX88 m mus musculus
18	516.5	24.6	152	2 Q6ZB95	Q6ZB95 homo sapien
19	502.5	23.9	309	1 CIW5_HUMAN	Q9t55 homo sapien
20	496.5	23.6	294	2 Q6X625	Q6X625 homo sapien
21	455	21.7	262	2 Q6X623	Q6X623 homo sapien
22	450	21.4	322	2 Q6X624	Q6X624 homo sapien
23	423.5	20.6	448	2 Q6PF03	Q6PF03 brachydanio
24	427	20.3	499	1 CIW5_HUMAN	Q9279 homo sapien
25	413	19.7	341	2 Q8H2T2	Q9JJK62 bos taurus
26	412.5	19.6	502	2 Q8JJK62	Q9JJK62 m potassium channel
27	409.5	19.5	257	2 Q8OKE0	Q8OKE0 mus musculus
28	406.5	19.4	307	2 Q8OIT4	Q8OIT4 xenopus laevis
29	390	19.0	184	2 Q8NAV5	Q8NAV5 homo sapien
30	393	18.7	332	1 CIW8_HUMAN	Q96154 homo sapien
31	380	18.1	336	2 Q8R454	Q8R454 cavia porcellus

#### ALIGNMENTS

RESULT 1		PRELIMINARY:		PRT: 411 AA.	
ID	Q9NRT2	ID	Q9NRT2;	PRELIMINARY:	
AC		AC	Q9NRT2;		
DT	01-OCT-2000	DT	01-OCT-2000	(TREMBLrel. 15, Created)	
DT	01-OCT-2000	DT	01-OCT-2004	(TREMBLrel. 15, Last sequence update)	
DT	25-OCT-2004	DT	25-OCT-2004	(TREMBLrel. 28, Last annotation update)	
DE	Two-pore domain potassium channel TREK-1 (potassium channel, subfamily K, member 2).	DE	K, member 2).		
GN	Name=TREK-1; Synonyms=KCNK2;	GN	Homo sapiens (Human)		
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCI TaxID=9606;	OS			
RN	SEQUENCE FROM N.A.	RN			
RP	TLSUB=brain;	RP			
RC	MEDLINE=20244931; PubMed=10784345;	RC			
RX	MEDLINE=22388257; PubMed=12477322; DOI=10.1073/pnas.242603899;	RX			
RA	Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schulz G.D., Altenschul S.F., Zeeberg B., Buetow K.H., Schaeffer C.F., Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Shapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Tsohlyabi S., Carninci P., Prange C., Raha S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mullany S.J., Bobak S.A., McKernan K.J., Malek J.A., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalick U., Smailus D.E., Jones S.J., Marra M.A.; Generation and initial analysis of more than 15,000 full-length human RT and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	RA			
RC	SEQUENCE FROM N.A.	RC			
RT	TLSUB=PCR rescued clones;	RT			
RA	Meadows H.J., Berham C.D., Cairns W., Gloger I.S., Jennings C., Medhurst A.D., Murdock P., Chapman C.G.;	RA			
RT	"Cloning, localisation and functional expression of the human orthologue of the TREK-1 potassium channel.", Pflugers Arch. 439:714-722(2000).	RT			
RL	[1]	RL			
RN	[2]	RN			
RP	SEQUENCE FROM N.A.	RP			
RC	TLSUB=PCR rescued clones;	RC			
RX	MEDLINE=22388257; PubMed=12477322; DOI=10.1073/pnas.242603899;	RX			
RA	Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schulz G.D., Altenschul S.F., Zeeberg B., Buetow K.H., Schaeffer C.F., Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Shapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Tsohlyabi S., Carninci P., Prange C., Raha S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mullany S.J., Bobak S.A., McKernan K.J., Malek J.A., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalick U., Smailus D.E., Jones S.J., Marra M.A.; Generation and initial analysis of more than 15,000 full-length human RT and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	RA			
RC	SEQUENCE FROM N.A.	RC			
RT	TLSUB=PCR rescued clones;	RT			
RA	Straubberg R.; Submits to the EMBL/GenBank/DDBJ databases.	RA			
CC	-1 SIMILARITY: Belongs to the two pore domain potassium channel (TC 1.A.1.8) family.	CC			

DR	GO; GO:0016021; C:integral to membrane; IEA.
DR	GO; GO:0016021; C:integral to membrane; IEA.
DR	GO; GO:0005216; F:ion channel activity; IEA.
DR	GO; GO:0005216; F:ion channel activity; IEA.
DR	GO; GO:0005267; F:potassium channel activity; IEA.
DR	GO; GO:0008811; F:potassium ion transport; IEA.
DR	GO; GO:0006813; F:potassium ion transport; IEA.
DR	InterPro; IPR003280; K+channel_2pore.
DR	InterPro; IPR001622; K+channel_pore.
DR	InterPro; IPR003976; Trek channel.
DR	PRINTS; PR01333; 2POREKCHANNEL.
DR	PRINTS; PR01499; TREKCHANNEL.
KW	Ion transport; Ionic channel; Transmembrane; Transport.
SEQUENCE	411 AA; 45494 MW; FDE4OCAB21B42A1C CR64;
Query Match	99.0%; Score 2079; DB 2; Length 411;
Best Local Similarity	99.0%; Pred. No. 1..7e-133;
Matches	410; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy	1 MAAPDLDPKSAAQNSKPRLSFSTKPTVLASRVEDDTINMKWKTIVSTIFLVVVLYLII 60
Db	1 MAAPDLDPKSAAQNSKPRLSFSTKPTVLASRVEDDTINMKWKTIVSTIFLVVVLYLII 60
Qy	61 GATVFKALEQPHESQRTTIVQKQTFISQHSCVNSTELDELQIPLGNT 120
Db	61 GATVFKALEQPHESQRTTIVQKQTFISQHSCVNSTELDELQIPLGNT 120
Qy	121 SNOISHWLGSSEFFAGTVITIGFGNISPRTEGGKFCIYALLGIPLFGLLAGYDQ 180
Db	121 SNOISHWLGSSEFFAGTVITIGFGNISPRTEGGKFCIYALLGIPLFGLLAGYDQ 180
Qy	181 LGTIFGRGIAKVEDTFLKWNVSQTKRIISTILFVGCVLFLVALPAIIFKHIEGMSALD 240
Db	181 LGTIFGRGIAKVEDTFLKWNVSQTKRIISTILFVGCVLFLVALPAIIFKHIEGMSALD 240
Qy	181 LGTIFGRGIAKVEDTFLKWNVSQTKRIISTILFVGCVLFLVALPAIIFKHIEGMSALD 240
Db	181 LGTIFGRGIAKVEDTFLKWNVSQTKRIISTILFVGCVLFLVALPAIIFKHIEGMSALD 240
Qy	241 AIFYVVITLTIGFGDYAGGSDEIYLDFYKPVWWFLVLYGLAYFAAVLSMIGDWLRVIS 300
Db	241 AIFYVVITLTIGFGDYAGGSDEIYLDFYKPVWWFLVLYGLAYFAAVLSMIGDWLRVIS 300
Qy	301 KTKKEEVGEFRHAENTANTAEFKETTRRLSVETIDKFQRATS1KRKLSAELAGHNQ 360
Db	301 KTKKEEVGEFRHAENTANTAEFKETTRRLSVETIDKFQRATS1KRKLSAELAGHNQ 360
Qy	361 ELTPCRRTLSVNLHTNERDVLPPLKTESITYNLTPHAGEEIAVHENIK 411
Db	361 ELTPCRRTLSVNLHTNERDVLPPLKTESITYNLTPHAGEEIAVHENIK 411
RESULT 3	CIW2_HUMAN STANDARD; PRT; 426 AA.
ID	CIW2_HUMAN STANDARD; PRT; 426 AA.
AC	Q9UNE3; Q9UNE3;
DT	16-OCT-2001 (Rel. 40, Created)
DT	16-OCT-2001 (Rel. 40, Last sequence update)
DT	05-JUL-2004 (Rel. 44, Last annotation update)
DE	Potassium channel subfamily K member 2 (Outward rectifying potassium channel protein TREK-1) (TREK-1 K+ channel subunit) (Two-pore channels)
DE	potassium channel TRPC1.
GN	Name=CNK2; Synonyms=TREK, TREK1; Homo sapiens (Human).
OS	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC	
NCBI_TaxID	9606; NCBI_TaxID=9606;
RN	[1] SEQUENCE FROM N.A.
RN	MEDLINE=99254548; PubMed=10321245; DOI=10.1038/8004;
RD	Patel A.J., Honore B., Lesage F., Fink M., Lazardski M.; "Inhalational anesthetics activate two-pore-domain background K+ channels"; Nat. Neurosci. 2:422-426(1999).
RN	[2] SEQUENCE FROM N.A.
RX	TISSUE=Adrenal cortex;
RX	MEDLINE=22370953; Published=12368289; DOI=10.1074/jbc.M207233200;
RA	Eyreart J.J., Xu L., Dantini S., Enyeart J.A.; "An ACTH- and ATP-regulated background K+ channel in adrenocortical cells is 'TREK-1'; J. Biol. Chem. 277:49186-49199 (2002).
CC	-; SIMILARITY: Belongs to the two pore domain potassium channel (TC 1.A.1.8) family.
CC	(TC 1.A.1.8) family.
DR	Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.



Qy	1 MAAPDLDPKSAAQNSKPRLSFSTKPTVLASRVEDDTINTMKWKTIVSTIFLVVLYLI 60	CC -!- MISCELLANEOUS: Inhibited by barium. Activated by volatile general anaesthetics such as chloroform, diethyl ether, halothane and isoflurane.
Db	4 VAPDLDPKSAQNSKPRLSFSSKPTVLASRVEDDTINTMKWKTIVSTIFLVVLYLI 63	CC -!- SIMILARITY: Belongs to the two pore domain potassium channel (TC 1.A.1.8) family.
Qy	61 GATVFKAQEPIISORTIVIQKQTTSQHCVNSTDELQIQQVAINAGTIPLGNT 120	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial purposes requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
Db	64 GATVFKAQEPIISORTIVIQKQTTSQHCVNSTDELQIQQVAINAGTIPLGNS 123	CC
Qy	121 SNOQSHDLGSFFFACTVITIGFNISSPRTEGGKLFCITYALIGIPLGF-LAGVGQ 180	CC
Db	124 SNOQSHDLGSFFFACTVITIGFNISSPRTEGGKLFCITYALIGIPLGF-LAGVGQ 183	CC
Qy	181 LGTIFGKGIAKYBDFIKWVNSQTKRIRIISTIIFLGCVLEVALPAIIFKHIEGMNALD 240	CC
Db	184 LGTIFGKGIAKYBDFIKWVNSQTKRIRIISTIIFLGCVLEVALPAIIFKHIEGMNALD 243	CC
Qy	241 AYFVWITLTIGFGDYAGGSDIEYDFYKEVWWFWLVLGLAYFAVLMSMIGDWLRVIS 300	DR MGD; MGI:109366; Kcnk2.
Db	244 AYFVWITLTIGFGDYAGGSDIEYDFYKEVWWFWLVLGLAYFAVLMSMIGDWLRVIS 303	DR GO; GO:0008076; C: voltage-gated potassium channel complex; IDA.
Qy	301 KTKKEEVEFRAHAENTANTAEFKETRRLSVEYDKEFQRTSJKRKLSAELAGHNQ 360	DR GO; GO:0005249; P: voltage-gated potassium channel activity; IDA.
Db	304 KTKKEEVEFRAHAENTANTAEFKETRRLSVEYDKEFQRTSJKRKLSAELAGHNQ 363	DR GO; GO:0007186; P: G-protein coupled receptor protein signalin.. . ; IDA.
Qy	361 ELTPCRRTLSVNLTHNLEDVLPPLKTESIVYLPHCAGEIAVENIK 411	DR InterPro; IPR003280; K+channel_pore.
Db	364 ELTPCRRTLSVNLTHSREVPPLKESIVYLPHCAGEDIAVENIK 414	DR InterPro; IPR003976; K+channel_pore.
<hr/>		
RESULT 5		
CLW2_MOUSE	AC P97438	Best Local Similarity 97.2%; Score 2041; DB 1;
ID	CD2_MOUSE	Matches 395; Conservative 12; Mismatches 4; Indels 0; Gaps 0;
AC	CIV2_MOUSE	Standard; PRT; 411 AA.
DT	16-OCT-2001 (Rel. 40, Created)	
DT	16-OCT-2001 (Rel. 40, Last sequence update)	
DT	05-JUL-2004 (Rel. 44, Last annotation update)	
DB	Potassium channel subfamily K member 2 (outward rectifying potassium channel protein TREK-1) (Two-pore potassium channel TPKC1)	
DE	K+	
DE	channel subunit.	
GN	Name=kcnk2;	
OS	Mus musculus (Mouse)	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OC		
NCBI_TaxID=10090;	RN [1]	
RP	SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.	
RC	TISSUE=Brain;	
RX	Medline=97157476; PubMed=9003761;	
RA	Fink M., Duprat F., Lescage F., Reye R., Romey G., Heurteaux C., Lazdunski M.;	
RT	"Cloning, functional expression and brain localization of a novel unconventional outward rectifier K <sup>+</sup> channel.";	
RT	EMBO J. 15: 6854-6862 (1996). [2]	
RP	REVISIONS.	
RC	Fink M., Duprat F., Lescage F., Reye R., Romey G., Heurteaux C., Lazdunski M.;	
RA	Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.	
RN	[3]	
RP	ACTIVATION.	
RX	Medline=99254548; PubMed=10321245; DOI=10.1038/8084;	
RA	"Inhalational anaesthetics activate two-pore-domain background K <sup>+</sup> channels.";	
RT	Nat. Neurosci. 2:422-426 (1999).	
CC	-!- FUNCTION: Outward rectifying potassium channel.	
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).	
CC	-!- TISSUE SPECIFICITY: High expression in brain and lung. Also detected in kidney, heart and skeletal muscle. Not detected in liver. In the brain, highest expression in olfactory bulb, hippocampus and cerebellum.	
CC		
Qy	1 MAAPDLDPKSAAQNSKPRLSFSTKPTVLASRVEDDTINTMKWKTIVSTIFLVVLYLI 60	CC -!- MISCELLANEOUS: Inhibited by barium. Activated by volatile general anaesthetics such as chloroform, diethyl ether, halothane and isoflurane.
Db	4 VAPDLDPKSAQNSKPRLSFSSKPTVLASRVEDDTINTMKWKTIVSTIFLVVLYLI 63	CC -!- SIMILARITY: Belongs to the two pore domain potassium channel (TC 1.A.1.8) family.
Qy	61 GATVFKAQEPIISORTIVIQKQTTSQHCVNSTDELQIQQVAINAGTIPLGNT 120	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial purposes requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
Db	64 GATVFKAQEPIISORTIVIQKQTTSQHCVNSTDELQIQQVAINAGTIPLGNS 123	CC
Qy	121 SNOQSHDLGSFFFACTVITIGFNISSPRTEGGKLFCITYALIGIPLGF-LAGVGQ 180	DR MGD; MGI:109366; Kcnk2.
Db	124 SNOQSHDLGSFFFACTVITIGFNISSPRTEGGKLFCITYALIGIPLGF-LAGVGQ 183	DR GO; GO:0008076; C: voltage-gated potassium channel complex; IDA.
Qy	181 LGTIFGKGIAKYBDFIKWVNSQTKRIRIISTIIFLGCVLEVALPAIIFKHIEGMNALD 240	DR GO; GO:0005249; P: voltage-gated potassium channel activity; IDA.
Db	184 LGTIFGKGIAKYBDFIKWVNSQTKRIRIISTIIFLGCVLEVALPAIIFKHIEGMNALD 243	DR GO; GO:0007186; P: G-protein coupled receptor protein signalin.. . ; IDA.
Qy	241 AYFVWITLTIGFGDYAGGSDIEYDFYKEVWWFWLVLGLAYFAVLMSMIGDWLRVIS 300	DR InterPro; IPR003280; K+channel_pore.
Db	244 AYFVWITLTIGFGDYAGGSDIEYDFYKEVWWFWLVLGLAYFAVLMSMIGDWLRVIS 303	DR InterPro; IPR003976; K+channel_pore.
Qy	301 KTKKEEVEFRAHAENTANTAEFKETRRLSVEYDKEFQRTSJKRKLSAELAGHNQ 360	DR PRINTS; PRO1333; 2PORECHANNEL.
Db	304 KTKKEEVEFRAHAENTANTAEFKETRRLSVEYDKEFQRTSJKRKLSAELAGHNQ 363	DR PRINTS; PRO1499; TREKCHANNEL.
Qy	361 ELTPCRRTLSVNLTHNLEDVLPPLKTESIVYLPHCAGEIAVENIK 411	DR Glycoprotein; Ion transport; Ionic channel; Potassium channel.
Db	364 ELTPCRRTLSVNLTHSREVPPLKESIVYLPHCAGEDIAVENIK 414	DR Potassium channel; Transmembrane; Transport; Voltage-gated channel.
Qy	301 KTKKEEVEFRAHAENTANTAEFKETRRLSVEYDKEFQRTSJKRKLSAELAGHNQ 360	DR KW Potassium channel; Transmembrane; Transport; Voltage-gated channel.
Db	304 KTKKEEVEFRAHAENTANTAEFKETRRLSVEYDKEFQRTSJKRKLSAELAGHNQ 363	DR KW Potassium channel; Transmembrane; Transport; Voltage-gated channel.
Qy	361 ELTPCRRTLSVNLTHNLEDVLPPLKTESIVYLPHCAGEIAVENIK 411	DR CYTOSM
Db	364 ELTPCRRTLSVNLTHSREVPPLKESIVYLPHCAGEDIAVENIK 414	DR CYTOSM
Qy	301 KTKKEEVEFRAHAENTANTAEFKETRRLSVEYDKEFQRTSJKRKLSAELAGHNQ 360	DR FT DOMAIN 1 46
Db	304 KTKKEEVEFRAHAENTANTAEFKETRRLSVEYDKEFQRTSJKRKLSAELAGHNQ 363	DR FT DOMAIN 1 47
Qy	361 ELTPCRRTLSVNLTHNLEDVLPPLKTESIVYLPHCAGEIAVENIK 411	DR FT DOMAIN 1 55
Db	364 ELTPCRRTLSVNLTHSREVPPLKESIVYLPHCAGEDIAVENIK 414	DR FT DOMAIN 1 57
Qy	301 KTKKEEVEFRAHAENTANTAEFKETRRLSVEYDKEFQRTSJKRKLSAELAGHNQ 360	DR FT TRANSMEM 155
Db	304 KTKKEEVEFRAHAENTANTAEFKETRRLSVEYDKEFQRTSJKRKLSAELAGHNQ 363	DR FT TRANSMEM 177
Qy	361 ELTPCRRTLSVNLTHNLEDVLPPLKTESIVYLPHCAGEIAVENIK 411	DR FT TRANSMEM 207
Db	364 ELTPCRRTLSVNLTHSREVPPLKESIVYLPHCAGEDIAVENIK 414	DR FT TRANSMEM 228
Qy	301 KTKKEEVEFRAHAENTANTAEFKETRRLSVEYDKEFQRTSJKRKLSAELAGHNQ 360	DR FT DOMAIN 238
Db	304 KTKKEEVEFRAHAENTANTAEFKETRRLSVEYDKEFQRTSJKRKLSAELAGHNQ 363	DR FT DOMAIN 268
Qy	361 ELTPCRRTLSVNLTHNLEDVLPPLKTESIVYLPHCAGEIAVENIK 411	DR FT DOMAIN 273
Db	364 ELTPCRRTLSVNLTHSREVPPLKESIVYLPHCAGEDIAVENIK 414	DR FT DOMAIN 293
Qy	301 KTKKEEVEFRAHAENTANTAEFKETRRLSVEYDKEFQRTSJKRKLSAELAGHNQ 360	DR FT DOMAIN 294
Db	304 KTKKEEVEFRAHAENTANTAEFKETRRLSVEYDKEFQRTSJKRKLSAELAGHNQ 363	DR FT DOMAIN 311
Qy	361 ELTPCRRTLSVNLTHNLEDVLPPLKTESIVYLPHCAGEIAVENIK 411	DR FT DOMAIN 354
Db	364 ELTPCRRTLSVNLTHSREVPPLKESIVYLPHCAGEDIAVENIK 414	DR FT DOMAIN 355
Qy	301 KTKKEEVEFRAHAENTANTAEFKETRRLSVEYDKEFQRTSJKRKLSAELAGHNQ 360	DR FT CARBOHYD 95
Db	304 KTKKEEVEFRAHAENTANTAEFKETRRLSVEYDKEFQRTSJKRKLSAELAGHNQ 363	DR FT CARBOHYD 119
Qy	361 ELTPCRRTLSVNLTHNLEDVLPPLKTESIVYLPHCAGEIAVENIK 411	DR FT CARBOHYD 119
Db	364 ELTPCRRTLSVNLTHSREVPPLKESIVYLPHCAGEDIAVENIK 414	DR SEQ SEQUENCE 45297 MW; 8F976DD103EPA05 CRC64;
Qy	301 KTKKEEVEFRAHAENTANTAEFKETRRLSVEYDKEFQRTSJKRKLSAELAGHNQ 360	DR Query Match Best Local Similarity 97.2%; Score 2041; DB 1;
Db	304 KTKKEEVEFRAHAENTANTAEFKETRRLSVEYDKEFQRTSJKRKLSAELAGHNQ 363	DR Matches 395; Conservative 12; Mismatches 4; Indels 0; Gaps 0;
Qy	1 MAAPDLDPKSAAQNSKPRLSFSTKPTVLASRVEDDTINTMKWKTIVSTIFLVVLYLI 60	Qy 1 MAAPDLDPKSAAQNSKPRLSFSTKPTVLASRVEDDTINTMKWKTIVSTIFLVVLYLI 60
Db	1 MAAPDLDPKSAAQNSKPRLSFSSKPTVLASRVEDDSAINTMKWTIVSTIFLVVLYLI 60	Qy 1 MAAPDLDPKSAAQNSKPRLSFSSKPTVLASRVEDDSAINTMKWTIVSTIFLVVLYLI 60
Qy	61 GATVFKAQEPIISORTIVIQKQTTSQHCVNSTDELQIQQVAINAGTIPLGNT 120	Qy 61 GATVFKAQEPIISORTIVIQKQTTSQHCVNSTDELQIQQVAINAGTIPLGNT 120
Db	61 GATVFKAQEPIISORTIVIQKQTTSQHCVNSTDELQIQQVAINAGTIPLGNS 120	Qy 61 GATVFKAQEPIISORTIVIQKQTTSQHCVNSTDELQIQQVAINAGTIPLGNS 120
Qy	121 SNOQSHDLGSFFFACTVITIGFGDYAGGSDIEYDFYKEVWWFWLVLGLAYFAVLMSMIGDWLRVIS 300	Db 121 SNOQSHDLGSFFFACTVITIGFGDYAGGSDIEYDFYKEVWWFWLVLGLAYFAVLMSMIGDWLRVIS 300
Db	124 AYFVWITLTIGFGDYAGGSDIEYDFYKEVWWFWLVLGLAYFAVLMSMIGDWLRVIS 303	Db 124 AYFVWITLTIGFGDYAGGSDIEYDFYKEVWWFWLVLGLAYFAVLMSMIGDWLRVIS 303
Qy	181 LGTIFGKGIAKYBDFIKWVNSQTKRKLIASTIIFLGCVLFVALPAIIFKHIEGMNALD 240	Qy 181 LGTIFGKGIAKYBDFIKWVNSQTKRKLIASTIIFLGCVLFVALPAIIFKHIEGMNALD 240
Db	181 LGTIFGKGIAKYBDFIKWVNSQTKRKLIASTIIFLGCVLFVALPAVIFKHIEGMNALD 240	Db 181 LGTIFGKGIAKYBDFIKWVNSQTKRKLIASTIIFLGCVLFVALPAVIFKHIEGMNALD 240
Qy	241 AYFVWITLTIGFGDYAGGSDIEYDFYKEVWWFWLVLGLAYFAVLMSMIGDWLRVIS 300	Qy 241 AYFVWITLTIGFGDYAGGSDIEYDFYKEVWWFWLVLGLAYFAVLMSMIGDWLRVIS 300
Db	244 AYFVWITLTIGFGDYAGGSDIEYDFYKEVWWFWLVLGLAYFAVLMSMIGDWLRVIS 303	Db 244 AYFVWITLTIGFGDYAGGSDIEYDFYKEVWWFWLVLGLAYFAVLMSMIGDWLRVIS 303
Qy	301 KTKKEEVEFRAHAENTANTAEFKETRRLSVEYDKEFQRTSJKRKLSAELAGHNQ 360	Qy 301 KTKKEEVEFRAHAENTANTAEFKETRRLSVEYDKEFQRTSJKRKLSAELAGHNQ 360
Db	304 KTKKEEVEFRAHAENTANTAEFKETRRLSVEYDKEFQRTSJKRKLSAELAGHNQ 363	Db 304 KTKKEEVEFRAHAENTANTAEFKETRRLSVEYDKEFQRTSJKRKLSAELAGHNQ 363
Qy	361 ELTPCRRTLSVNLTHNLEDVLPPLKTESIVYLPHCAGEIAVENIK 411	Qy 361 ELTPCRRTLSVNLTHSREVPPLKESIVYLPHCAGEDIAVENIK 411





DE 10 (OUTWARD RECTIFYING POTASSIUM CHANNEL PROTEIN TREK-2) (TREK-2 K+  
DE CHANNEL SUBUNIT) homolog.  
OS Mus musculus (Mouse).  
OC Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10900;  
RN [1] SEQUENCE FROM N.A.  
RP STRAIN=C57BL/6J; TISSUE=Cerebellum;  
RX RA Carninci P., Hayashizaki Y.;  
RT "High-efficiency Full-length cDNA cloning.";  
RL Meth. Enzymol. 303:19-44 (1999).  
RN [2] SEQUENCE FROM N.A.  
RP STRAIN=C57BL/6J; TISSUE=Cerebellum;  
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
RA RIKEN FANTOM Consortium;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RN Nature 409:685-690(2001).  
RN [3] SEQUENCE FROM N.A.  
RP STRAIN=C57BL/6J; TISSUE=Cerebellum;  
RA The FANTOM Consortium,  
RA RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
60,770 full-length cDNAs.";  
RT RN 420:563-573 (2002).  
RN [4] SEQUENCE FROM N.A.  
RP STRAIN=C57BL/6J; TISSUE=Cerebellum;  
RX PubMed=11042159; DOI=10.1101/gr.145100;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RA "Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes.";  
RA Genome Res. 10:1617-1630 (2000).  
RN [5] SEQUENCE FROM N.A.  
RP STRAIN=C57BL/6J; TISSUE=Cerebellum;  
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sabaki N., Carninci P.,  
RA Akiyama J., Nishi K., Kitamura T., Tashiro H., Itoh M.,  
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishihine T., Harada A.,  
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
RA Yoneda Y., Ishikawa T., Togawa Y., Iwasa K., Tanaka T., Ohara E., Wakahiki M.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
RA "RIKEN integrated sequence analysis (RISA) system-384-format  
sequencing Pipeline with 384 multicapillary sequencer.";  
RT Genome Res. 10:1757-1771 (2000).  
RN [6] SEQUENCE FROM N.A.  
RP STRAIN=C57BL/6J; TISSUE=Cerebellum;  
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
RA Fukuda S., Puruno M., Hanagaki T., Hara A., Hashizume W.,  
RA Hayashida K., Hayatsu N., Haramoto K., Hiraoaka T., Hirozane T.,  
RA Hori F., Imotori K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
RA Kurihara C., Matsui J., Kojima Y., Kondo S., Konno H., Koya S.,  
RA Nishi K., Nomura K., Numazaki R., Miyazaki A., Murata M., Nakamura M.,  
RA Saitoh R., Saitoh H., Sakai C., Sakai K., Ohno M., Ohshiro N., Okazaki Y.,  
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
RA Tagawa A., Takahashi F., Takaku Akahira S., Takeda Y., Tanaka T.,  
RA Tomaru A., Toya T., Yasunishi A., Muzamatsu M., Hayashizaki Y.;  
RA Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
CC -1 SIMILARITY: Belongs to the two pore domain potassium channel  
(TC 1.A.1.8) family.  
EMBL; AKA082153; BA3842.1. -

DR GO:0006813; Pi:potassium ion transport; IEA.  
DR InterPro; IPR003280; K-channel\_2pore.  
DR InterPro; IPR001622; K-channel\_pore.  
DR IPD003976; TREK channel.  
PRNTS; PR0133; 2PORECHANNEL.  
PRNTS; PR0199; TREKCHANNEL.  
DR Ion transport; Ionic channel; Transmembrane; Transport.  
SQ SEQUENCE 535 AA; 59401 MW; 3E98E89F875C26BD CRC64;

Query Match 59.5%; Score 1249.5%; DB 2;  
Best Local Similarity 59.3%; Prod. No 2, 8e-76;  
Matches 252; Conservative 61; Mismatches 77; Indels 35; Gaps 7;

QY 2 AAPPLLDPKSA- AQNSKPRLSPLSTKPTVLAQSVESDT--TINVMKQKTVSTIFLYVVVL 56  
Db 20 AAPVCOPKSATNQHHFPLRLLSSRATVA-RMEGASGGLQTMVKWTKVVAIFVVVVV 78  
QY 57 YLIGATYPKALEOPHEPSQRTTIVIQKOTFISCHSCVNSTELDELQIVAAANAGILP 116  
Db 79 YLVVTGGLYRALBOPPEFESSQKNTIALEKAELFRDHICVSQPELETQHALDANAGVSP 138

QY 117 LGNTSNOISHWDLGSSFFPAGTYTTTGCNTRTEGSKFCITVYALGIPIFGFLIG 176  
Db 139 VGNSSNSSSHWDLGSAFFPAGTYTTGGINAIPSTEGKIFCILYAIFGIPLEGFLLG 198

QY 177 VGDOLGTIFGKGIAKVEDTPKINVSQTKIRIISTIIIFLFGCVTFVALPAIFKHIEGW 236  
Db 199 IGDLQGITFGKSTARVEKVFRKKQVSQTKIRVSTISLFLAGCTVFTTIPAVIKYIEGW 255

QY 237 SALDAIYFWVITLTGIGDYVAGG-SDIEYLDQYKPVWFWIWINGLAYFAAVLSMIGDW 295  
Db 259 TALESIYFWVVTILTGVGFDPVAGGNAGINYREWYKPLVWFWIWINGLAYFAAVLSMIGDW 318

QY 296 LRVTSKTKYEVGIFRAAENTVNTAEFKTRRLSEVYTDFKTFRQLKFORATSI---KRKLIS 351  
Db 319 LRVLSKTKYEVGIFRAAEWKAVTAEFTRRLSEVTFHDLQRATIRSMERRUG 378

QY 352 AELAGNNHQELTPQRTL-----SYNHLTNERDVLPPLLKTESTYLNGLT 396  
Db 379 LDQRQHSUDMLSLPSPKRSVFAALDTGRFRASSQSINRNPNNLRLKGP-----EQLT 429

QY 397 PHCAG 401  
Db 430 KHGGG 434

RESULT 10  
CIWA\_RAT STANDARD; PRT; 538 AA.  
ID CIWA\_RAT  
AC Q91IS4;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Potassium channel subfamily K member 10 (outward rectifying potassium channel protein TREK-2) (TREK-2 K+ channel subunit).  
DE Name=Kcnk10; Synonym=TREK2;  
OS Rattus norvegicus (Rat).  
OC Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
NCI\_TAXID=10116;  
RN RP SEQUENCE FROM N.A.  
MEDLINE=2029807; PubMed=10747911;  
RA Bang H., Kim Y., Kim D.;  
RA "TREK-2," a new member of the mechanosensitive tandem-pore K+ channel family.;  
RT RL J. Biol. Chem. 275:17412-17419 (2000).  
CC -1 FUNCTION: Outward rectifying potassium channel. Produces rapidly activating and non-inactivating outward rectifier K(+) currents.  
CC Activated by arachidonic acid and other naturally occurring unsaturated free fatty acids.  
CC -1 SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
CC -1 TISSUE SPECIFICITY: Expressed mainly in the cerebellum, spleen,

CC and testis.  
 CC - SIMILARITY: Belongs to the two pore domain potassium channel  
 (TC 1.A.1.8) family.

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 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (see <http://www.isb-sib.ch/announce/>  
 or send an email to license@isb-sib.ch).

CC EMBL; AF196365; AAF75132.1; -  
 DR InterPro; IPR003280; K+channel\_2pore.  
 DR InterPro; IPR016322; K+channel\_Pore.  
 DR PRINTS; PR01333; 2POREKCHANNEL.  
 DR PRINTS; PR01499; TREKCHANNEL.  
 KW Glycoprotein; Ion transport; Potassium; Transport; Voltage-gated channel.  
 KW Potassium channel; Transmembrane; Potassium; Transport; Voltage-gated channel.  
 FT DOMAIN 1 71 Cytoplasmic (Potential).  
 FT TRANSMEM 72 92 Potential.  
 FT DOMAIN 154 180 Pore-forming 1 (Potential).  
 FT TRANSMEM 182 202 Potential.  
 FT DOMAIN 203 233 Cycoplasmic (Potential).  
 FT TRANSMEM 234 254 Potential.  
 FT DOMAIN 263 294 Pore-forming 2 (Potential).  
 FT TRANSMEM 299 319 Potential.  
 FT DOMAIN 320 538 Cytoplasmic (Potential).  
 FT CARBOHYD 144 144 N-linked (GICNAC. . .) (Potential).  
 FT CARBOHYD 147 147 N-linked (GICNAC. . .) (Potential).  
 SEQUENCE 538 AA; 59800 MW; 1FF35F0AA52B97E4 CRC64;

Query Match 59.5%; Score 1249; DB 1; Length 538;  
 Best Local Similarity 63.7%; Pred. No. 3.le-76;  
 Matches 247; Conservative 55; Mismatches 64; Indels 22; Gaps 6;

Qy 2 AAPDLDPKSA --AQNSKPRLSFSKTPVLAQRVESDT--TINVMKKTVSTIFLVVL 56  
 Db 23 AAPPVQCQKSATGHHPPRLSSRATVVA.RMEGAQQGLQTWKVVAIFVVVV 81

Qy 57 YLTIGATYFKALEQPHETISQRTTIVIKOTFISQHSCVNSTELDELIQYVAANAGIIP 116  
 Db 82 YLVGGGLVERALEQPFESISQTKTIALEAFLRDHICWSPQLETUHQHALDADNAGVSP 141

Qy 117 LENTSNQSHWDLGSSPFGAGVTTIGFGNISPRTEGGKFCITAYLIGPLFGFLAG 176  
 Db 142 VGNNSNSSHWDLGSAFPFGAVTTIGGNLAPSTEGKFCILVAFGIPLGFLAG 201

Qy 177 VGDQLGTFGKTAKEVDFTIKWNVSQKIRLSTITFLFGCVLFVPAFLFHIEGW 236  
 Db 202 IGDQLTGFQSKTARVEKFVRKQVSQTKIRVISTILFLAGCIVFTTIPAVIFKYIEW 261

Qy 237 SALDAIYFWVITLTTIGFGDYAGG-SPIEYLDFYKPVWFMFLVGLAYFAAVLMSMIDW 295  
 Db 322 LRVLSKKTKEEVGEIKAKRAEWKANTVYEFTRRRLSEIHDCLQQAATR---SME-- 376

Qy 356 GHNQELTPCRRLTSVNLTNEBDVLP 383  
 Db 377 -----RRRIGLQDQRAHSIDMLSP 394

DE Potassium channel subfamily K member 10 (Outward rectifying potassium  
 DE channel protein TREK-2) (TREK-2 K+ channel subunit).  
 DC Name=KCNK10; Synonyms=TREK2;  
 OS Homo sapiens (Human); Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Eukaryota; Metazoa; Primates; Catarrhini; Hominoidea; Homo.  
 CC Mamalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 NCBI\_TAXID=9606;  
 RN [1] SEQUENCE FROM N.A. (ISOFORM A).  
 RP MEDLINE=10880510; PubMed=10880510; DOI=10.1074/jbc.M002822200;  
 RX Lesage F., Terrenoire C., Romeo G., Lazdunski M.;  
 RA "Human TREK-2, a 2P domain mechano-sensitive K+ channel with multiple  
 RT regulations by polyunsaturated fatty acids, lysophospholipids and Gs,  
 RT Gi, and Gq protein-activated receptors.";  
 RL J. Biol. Chem. 275:28398-28405(2000). *for kate*  
 RN [2] SEQUENCE FROM N.A. (ISOFORMS B AND C).  
 RP MEDLINE=21896087; PubMed=11897838;  
 RA Gu W., Schlitzthorl G., Hirsch J.R., Engels H., Karschin C.,  
 RA Karschin A., Dertf C., Steinlein O.K., Daut J.;  
 RA "Expression pattern and functional characteristics of two novel splice  
 RT variants of the two-pore-domain potassium channel TREK-2.";  
 RL J. Physiol. (Lond.) 539:657-668(2002).  
 CC -I- FUNCTION: Outward rectifying potassium channel. Produces rapidly  
 CC activating and non-inactivating outward rectifier K(+) currents.  
 CC Activated by arachidonic acid and other naturally occurring  
 CC unsaturated free fatty acids.  
 CC -I- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -I- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=3;  
 CC Name=A; Synonyms=TREK2a;  
 CC IsoId=P57789-1; Sequence=Displayed;  
 CC Name=B; Synonyms=TREK2b;  
 CC IsoId=P57789-2; Sequence=VSP\_006697;  
 CC Name=C; Synonyms=TREK2c;  
 CC IsoId=P57789-3; Sequence=VSP\_006698;  
 CC -I- TISSUE SPECIFICITY: Abundantly expressed in pancreas and kidney  
 CC Isoform b is strongly expressed in kidney (primarily in the  
 CC proximal tubule) and pancreas, whereas isoform c is abundantly  
 CC expressed in brain.  
 CC -I- SIMILARITY: Belongs to the two pore domain potassium channel  
 CC (TC 1.A.1.8) family.  
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 CC or send an email to license@isb-sib.ch).

CC GO; GO:0005267; F:potassium channel activity; TAS.  
 DR EMBL; AF27989; AAG15191.1; -  
 DR EMBL; AF38539; AAL95705.1; -  
 DR InterPro; IPR003280; K+channel\_2pore.  
 DR InterPro; IPR001622; K+channel\_pore.  
 DR InterPro; IPR003976; Trek\_channel.  
 DR PRINTS; PRO1333; 2POREKCHANNEL.  
 DR PRINTS; PRO1499; TREKCHANNEL.  
 KW Potassium; Potassium channel; Transmembrane; Transport;  
 KW Voltage-gated channel.  
 FT DOMAIN 1 71 Cytoplasmic (Potential).  
 FT TRANSMEM 72 92 Potential.  
 DR DOMAIN 154 180 Pore-forming 1 (Potential).  
 FT TRANSMEM 203 233 Potential.  
 FT TRANSMEM 203 254 Cytoplasmic (Potential).  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)

RESULT 11  
 C1WA\_HUMAN  
 ID C1WA\_HUMAN  
 STANDARD: PRT; 538 AA.  
 AC P57789; Q8TDK7; Q8BB59;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)



GN Name=LOC446288; OS Xenopus laevis (African clawed frog). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipoideae; OC Xenopus. NCBI_TaxID=8355; RN [1] RP SEQUENCE FROM N.A. RC TISSUE-EYE; RX MEDLINE=2334112; PubMed=1245917; DOI=10.1002/dvdy.10174; RA Klein S.L.; Strausberg R.L.; Wagner L.; Pontius J.; Clifton S.W., Richardson P.; RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus initiative." RL Dev. Dyn. 225:384-391(2002). RN [2] RP SEQUENCE FROM N.A. RC TISSUE-EYE; RX PubMed=12477932; RA Straubhaar R.L.; Feingold E.B.; Grouse L.H.; Derge J.G.; Scherzer C.M.; Schuler G.D.; RA Klaushofer R.D.; Collins F.S.; Wagner J.; Shemesh C.M.; Schuler G.D.; RA Altschuler S.F.; Zeiberg B.; Buetow K.H.; Schaefer C.P.; Bhat N.K., RA Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Hsieh F., RA Diatchenko L.; Marusina K.; Farmer A.A.; Rubin G.M.; Hong L., RA Stapleton M.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Schatz T.E., RA Brownstein M.J.; Usdin T.B.; Toshiyuki S.; Carninci P.; Prange C., RA Raha S.S.; Loqueland N.A.; Peters G.J.; Abramson R.D.; Mullahay S.J., RA Bosak S.A.; McEwan P.J.; McKernan K.J.; Malek J.A.; Gunaratne P.H., RA Richards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.W., RA Villalon D.K.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A., RA Fahey J.; Heitton B.; Kettemann M.; Madan A.; Rodriguez S.; Sanchez A., RA Whiting M.; Madan A.; Young A.C.; Shevchenko Y.; Bouffard G.G., RA Blakesley R.W.; Touchman J.W.; Green E.D.; Dickson M.C., RA Rodriguez A.C.; Grimwood J.; Schmutz J.; Myers R.M.; Butterfield Y.S., RA Krzywinski M.I.; Skalska U.; Smailus D.E.; Schnurch A.; Schein J.E., RA Jones S.J.; Marras M.A.; RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002). RN [3] RP SEQUENCE FROM N.A. RC TISSUE-EYE; RA Klein S.; Gerhard D.S.; RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases. DR EMBL; BC080069; AAH80069.1; DR InterPro; IPR00280; K+channel_2pors. DR InterPro; IPR001622; K+channel_pore. DR PRINTS; PRO1333; 2POREKCHANNEL. DR PRINTS; PRO1499; TREKCHANNEL. FT NON-TER; 546 546 AA; SQ SEQUENCE 546 AA; 60977 MW; AF6CFB34AD34A06 CRC64;	Qy 257 YVAGG-SDIEYLDFFKPKVWWFWILVGLAYPAVLSMIGDWLRVISKKTKEEVGEFRHAA 315 :      :      :      :      :      :      :      :      :      :      :      :      :    Db 292 FVAGGNTDISREWPKPLWNVWILVGLAYPAVLSMIGDWLRVISKKTKEEVGEFRHAA 351 :      :      :      :      :      :      :      :      :      :      :      :      :    Qy 316 EWTANYTAEPKETRRLSVEYDKFORATSIKKSALAEAGLNHNQELTPCERTLSVNNHLT 375 :      :      :      :      :      :      :      :      :      :      :      :      :   : Db 352 EWKANTTAEPKETRRLSVEIHKDQRAATR--SMB-----RRRLGDQRA 396 :      :      :      :      :      :      :      :      :      :      :      :      :   : Qy 376 NERDVLPP 383 :      :      :      :      :      :      :      :      :      :      :      :      :   : Db 397 HSLDMILSP 404 :      :      :      :      :      :      :      :      :      :      :      :      :   : RN [4] RP SEQUENCE FROM N.A. (ISOFORM 14) ID CIWA_HUMAN STANDARD; AC Q9NYC8; Q96T94; DT 16-OCT-2001 (Rel. 40, Created) DT 16-OCT-2001 (Rel. 40, Last sequence update) DT 05-JUL-2004 (Rel. 44, Last annotation update) DE Potassium channel subfamily K member 4 (TWIK-related arachidonic acid- stimulated potassium channel protein) (TRAAK) (Two pore K+ channel KT4). DN Name=KCNK4; Synonyms=TRAAK; OS Homo sapiens (Human). OC Mammalia; Euteozoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Metazoa; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606; OX OX; RN [1] RP SEQUENCE FROM N.A. (ISOFORM 1). RN TISSUE=Brain; RC Tissue=Brain; RN TISSUE=Brain; PubMed=11042359; DOI=10.1016/S0167-328X(00)00183-2; RA Chapman C.G.; Meadows H.J.; Godden R.J.; Campbell D.A.; Duckworth M.; RA Kelbell R.E.; Murdoch P.R.; Randall A.D.; Reunie G.I.; Gloger I.S.; RA Lesage F.; Mangret F.; Lazdunski M.; RT "Cloning, localisation and functional expression of a novel human, RT cerebellum specific, two pore domain potassium channel."; RL Brain Res. Mol. Brain Res. 82:74-83(2000). RN [2] RP SEQUENCE FROM N.A. (ISOFORM 1). RC TISSUE=Frontal cortex; RN Gray A.T.; RA "Assignment of KCNK4 encoding the human potassium channel TRAAK to RT chromosome 11"; RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases. RN [3] RP SEQUENCE FROM N.A. (ISOFORM 1). RN TISSUE=Brain; PubMed=20231639; PubMed=10.1016/S0014-5793(00)01388-0; RA Ozaita A.; Vega-Saenz de Miera J.; RT "Cloning of two transcripts, HK4-1a and HK4-1b, from the human two- RT pore K+ channel gene KCNK4. Chromosomal localization, tissue RT distribution and functional expression."; RL Brain Res. Mol. Brain Res. 102:18-27(2002). RN [4] RP SPLICE ISOFORM(S) THAT ARE POTENTIAL NMN TARGET (S). RN SEQUENCE FROM N.A. (ISOFORMS 1 AND 2). RP MEDLINE=22178305; PubMed=12191490; DOI=10.1016/S0169-328X(02)00157-2; RA Ozaita A.; Vega-Saenz de Miera J.; RT "An unappreciated role for RNA surveillance"; RN "RESEARCH008.1-RESEARCH008.16"; RL Genome Biol. 5:RESEARCH008.1-RESEARCH008.16 (2004). CC -I- FUNCTION: Voltage insensitive, instantaneous, outwardly rectifying CC potassium channel. Outward rectification is reversed at high CC external K(+) concentrations (By similarity). CC -I- SUBUNIT: Homodimer (Potential). CC -I- SUBCELLULAR LOCATION: Integral membrane protein (Potential). CC -I- ALTERNATIVE PRODUCTS: CC Event=Alternative splicing; Named isoforms=2; Name=1; Synonyms=K14.1a; CC
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CC	IsoId=Q9NYGB-1; Sequence=displayed;
CC	Name=2; Synonyms=Kcn4.1b;
CC	IsoId=Q9NYGB-2; Sequence=VSP_006689;
CC	Codeon in the mRNA, leading to a premature stop
CC	Note=May be produced at very low levels due to a nonsense-mediated mRNA decay;
CC	-1- SIMILARITY: Belongs to the two pore domain potassium channel (TC 1.A.1.8) family.
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CC	SECRETION FROM N.A.
DR	EMBL; AF248242; MAG31731.1; ALT_INIT .
DR	EMBL; AF247042; AAF64062.1; ALT_INIT .
DR	EMBL; AF259500; AAK49369.1; .
DR	EMBL; AF259501; AAK49390.1; .
DR	GeneID: HGNC:6279; KCNK4.
DR	MIM: 605720; .
DR	GO: GO:0005267; P:potassium channel activity; TAS .
DR	GO: GO:0006843; P:potassium ion transport; TAS .
DR	InterPro: IPR003280; K+channel_2pore.
DR	InterPro: IPR001622; K+channel_pore.
DR	InterPro: IPR008074; TRAAK channel.
DR	PRINTS: PRO1333; 2PORECHANEL.
KW	Alternative splicing; Glycoprotein; Ion transport; Ionic channel; Potassium; Potassium channel; Transmembrane; Transport; Voltage-gated channel.
KW	Voltage-gated channel.
FT	DOMAIN 1 3
FT	TRANSMEM 4 24
FT	TRANSMEM 89 113
FT	TRANSMEM 118 138
FT	TRANSMEM 139 171
FT	TRANSMEM 172 192
FT	DOMAIN 197 221
FT	TRANSMEM 234 254
FT	TRANSMEM 255 393
FT	CARBOHYD 78 78
FT	CARBOHYD 82 82
FT	VARSPLIC 1 1
FT	POTENTIAL 2
FT	POTENTIAL 4
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FT	POTENTIAL 439
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FT	POTENTIAL 441
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FT	POTENTIAL 443
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FT	POTENTIAL 446
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FT	POTENTIAL 472
FT	POTENTIAL 473
FT	POTENTIAL 474
FT	POTENTIAL 475
FT	POTENTIAL 476
FT	POTENTIAL 477
FT	POTENTIAL 478
FT	POTENTIAL 479
FT	POTENTIAL 480
FT	POTENTIAL 481
FT	POTENTIAL 482
FT	POTENTIAL 483
FT	POTENTIAL 484
FT	

Query Match      Score 76.5;      DB 1;      Length 398;  
 Best Local Similarity      49.8%;      Pred. No. 1.9e-44;      Gaps 1;  
 Matches 142;      Conservative 57;      Mismatches 83;      Indels 3;

---

Qy      42 MKWKTUSTIFLVVVLIGATVKALEQPHESIORTTIVIQKOPTISCHSCVNTELDE 101  
 :|: :|: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:  
 Db      1 MRSTTLALLALVLLVSGALVFOALEQPHQQAQMDGRDQLRDPCVSOKSLED 60

Qy      102 LIQQTVAINAGIIP--LGNTSNQI SHWDLGSSPFAGTVITTGFGNISPRTEGGKF 158  
 :|: :|: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:  
 Db      61 FTKLIVAEALGGGANPETSWTNNHSSAANLGSAAFSGTTITTCGYGNTVLHTDAGRLF 120

Qy      159 CIYALLGIPPLGFILLAGVDOLGTIFKGIAKVEDTFKHNVSQPKIRIISTIFILFG 218  
 :|: |: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:  
 Db      121 CIFYALVGIPPLGMLLAGVDLGSILRGIGHIEIFLRKHVPPLVRSISAVLFLLIG 180

Qy      219 CVLFVALPAFLPKHIEGWSALDAIYFVVTITLTIGRSDYYAGGSDEIYLDFYKPVWFWI 278  
 :|: |: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:  
 Db      181 CILFVLTPTFVSYMESWSKLEAIYPVTVLTTVGFQDGTQNSPAYQPLWFWI 240

Qy      279 LVGLAYPAVLSMIGDMRLRVISKKTRKEVGEFRAHAEWTANVTA 323  
 :|: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:  
 Db      241 LFGLAYPAVSLTTIGNMLRAVSRRTAEMGGLTQAQASWTGTVTA 285

Search completed: July 13, 2005, 08:44:29  
 Job time : 96.9622 secs



A; Molecule type: DNA	
A; Residues: 1-330 <KIM>	
A; Cross-references: GB:ALL110522	
C; Comment: This protein, a new member of the tandem-pore K <sup>+</sup> channel family with four transmembrane segments, but does not produce a functional plasma membrane K <sup>+</sup> current by itself	
C; GenBank: C; GenBank:	
A; Gene: task-5	
A; Map position: 20q12	
C; Keywords: transmembrane protein	
C; Status: Predicted <TM51>	
F; F; 7-30/Domain: transmembrane segment #status predicted <TM51>	
F; F; 107-118/Domain: transmembrane segment #status predicted <TM52>	
F; F; 129-135/Region: hydrophobic cytoplamic Linker #status predicted	
F; F; 156-180/Domain: transmembrane segment #status predicted <TM53>	
F; F; 220-240/Domain: transmembrane segment #status predicted <TM54>	
Query Match 16.5%; Score 347.5.; DB 2; Length 330;	
Best Local Similarity 34.9%; Pred. No. 1.4e-20;	
Matches 91; Conservative 42; Mismatches 95; Indels 33; Gaps 9;	
Qy 50 IFLVVVLYLIGATYVKALEQPHRISORTIVIQOKTISO---HSCVNSTELDELJQQI 106	
Db 11 LVLCTCYLLGVAFDALESEAS-SGRORLIVQRRKGFSADYRELRLAQ- 68	
Qy 107 VAAANAGITIPLGNTSNQIHLWDDGSSPFAGNTVTTTGFGNISPRTBGKFCITAYALG 166	
Db 69 AEPRHAG-----RQWKFPGSFYFAITVTTTGYGHAPGTDSGVFKCMFVALLG 117	
Qy 167 IPLRGFLACVGQDGDTGKGKIAKVEDTF-I-KWNVSQTKIRIISTIIFLFGCVLFVAL 225	
Db 118 IPLTIVTPTFSLGEIRNAVVRLLIAKCCGLERWTCTSE---NLVAGLILACATYL 173	
Qy 226 PAIPKHHGWSALDAIYFVVTIITLTCGFDYYAGGSDEIYLDFFYKPVVWF--WILVGLI 282	
Db 174 GAVAFSHFEGFWTFPHAYYYCFTTTGDFDVALQSG-EALQRKUPYVAEFSFLYIILGL 232	
Qy 283 AYFARVLSM-----GDW 295	
Db 233 TVIGAFNLNVLRFLIVASADW 253	
RESULT 3	
T43509 probable potassium channel chain n2P38 - <i>Caenorhabditis elegans</i>	
C;Species: <i>Caenorhabditis elegans</i>	
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004	
C;Accession: T43509	
A;Description: Potassium Channels in <i>C. elegans</i> .	
A;Reference number: 222450	
A;Status: preliminary; translated from GB/EMBL/DDBJ	
A;Cross-references: UNIPROT:017185; ENBL:AF083652; PIDN: AAC32863.1	
Query Match 16.4%; Score 345.; DB 2; Length 329;	
Best Local Similarity 33.7%; Pred. No. 2.2e-20;	
Matches 93; Conservative 56; Mismatches 93; Indels 34; Gaps 11;	
Qy 42 MKWKTIVTPIFLVV--VLYLIGATYVKALEQPHISORTIVIQOKTISOHCVNSTL 99	
Db 1 MKRQNRITSLIVTPTLYLGVAFDALETEENILQRKLVQVEREKKTKNMNSNA-DY 59	
Qy 100 DELIQQIVAAI--NAGIIPIGNTSNQIHSWDLGSSEFFAGTVITITGFGNISPRTEGGKI 157	
Db 60 EILRIVATIVSPVHAGY-----QMFKSCAFYPATVTTIGHSPMTDAGKV 108	
Qy 158 PCITVALLGGLPFLGFLLAGYGDQIUTIFKGKIAKVEDTFIKWNSQISKIRIISTIIFL 217	
Db 109 PCMLYALAGPLGLIMFOISGERNTFAKLL---RFIRRAAKGPVITSSDILIFCT 163	
Qy 218 GC-YLVFVALPAIFIYKHIEGWSALDAIYFVVTIITLIGFDYVA---GSS---DIEYLDFY 270	

Db	164	GNCGLLFFGGATMFSSEYENWTFDAAVYCFVTLTTGRDVAALQKRSLSLQTQFYY-FF	222
Qy	271	KPVVFWFLILGLAYFAAVLMSIGDWLRVISCKKEE	306
Db	223	SIV--FILEGLTVISAMNL--VIRFLTMNTED	253
<b>RESULT 4</b>			
outward rectifier potassium channel homolog twk-23 - <i>Caenorhabditis elegans</i>			
C;Species:	<i>Caenorhabditis elegans</i>		
C;Date:	29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004		
C;Accession:	T32347		
R;Murray, J.; Wohldmann, P.; O'Neal, D.			
A;Cross-references:	UNIPROT:O17185; EMBL:AF025454; PIDN: AAC71151.1; GSPDB: GN000		
A;Experimental source:	strain Bristol N2; Clone F34D6		
A;Reference number:	221153		
A;Accession:	T32347		
A;Status: preliminary; translated from GB/EMBL/DBJ			
A;Molecule type: DNA			
A;Residues: 1-336 <MDR>			
A;Gene: twk-23; CESP:F34D6.3			
A;Map position: 2			
A;Introns: 44/3; 102/1; 136/1; 180/1; 207/1; 265/2; 296/3			
Query Match	15.8%	Score 331.5; DB 2; Length 336;	
Best Local Similarity	32.9%	Prod. No. 2.8e-19; Length 336;	
Matches	93;	Conservative 56; Mismatches 93; Indels 41; Gaps 12;	
Qy	42	MKWTKTSTTFLVV--VLYLIGATVKALEQPHBISQ-----RTTIVQIKQDPIQSNS	92
Db	1	MQRQNITSLIVCTYLLVGRAVEELTEENILQVRGLGPRLKQVRVREKLKTY	100
Qy	93	CVNSTELDELQIVAAI--NAGLIPLGNTSNQIWHDLGSSPFAGTWTITGFGNISP	150
Db	61	MSPNA-DVELEATIVKSYPHKAGY-----QWKFGSAYFATVITIGYGHSTPP	108
Qy	151	RTEGGKFCIYLALGIPFGLLAGVGQDQLGTFKGIAKVEDTFTKWNVSQTKIRIL	210
Db	109	MTDAGKVFCMLYALAGIPLGLIMQSGERMTFAKUL-----RFIRRAAGKOPPIVTSS	163
Qy	211	TTFILFLFC--VLFVALPALIFKHIGNSALADITYFWVITLTGTFGDVVA---GS---D	263
Db	164	DLIIFTCWGGHLIIFPGDFMFSSYERYNFYDAAVYCPVLTITLGTFGDVVAQRGSLQTO	223
Qy	264	IKEYDFYKPVVWWFVWLGLAYFAAVLMSIGDWLRVISCKTEE	306
Db	224	PEYV-FFSFLV--FILEGLTVISAMNL--VIRFLTMNTED	260
<b>RESULT 5</b>			
potassium channel protein - fruit fly ( <i>Drosophila melanogaster</i> )			
C;Species:	<i>Drosophila melanogaster</i>		
C;Date:	13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004		
C;Accession:	T13807		
R;Goldstein, S.A.; Price, L.A.; Rosenthal, D.N.; Pausch, M.H.			
Proc. Natl. Acad. Sci. U.S.A. 93, 11256-11261, 1996			
A;Title: ORK1, a potassium-selective leak channel with two pore domains cloned			
A;Reference number: 211770; PMID: 97075152; PMID: 8917578			
A;Accession: T13807			
A;Status: preliminary; translated from GB/EMBL/DBJ			
A;Molecule type: mRNA			
A;Residues: 1-1001 <GOL>			
A;Cross-references:	UNIPROT:Q94526; EMBL:U55321; NID:q3808067; PID:93808068; PI		
C;Genetics:			
A;Gene: ORK1			
A;Cross-references:	FlyBase:FBgn0017561		





A;Map Position: 3 A;Introns: 47/2; 82/2; 106/3; 151/1; 220/1; 260/3; 370/3 A;Note: Y3986B.F	Db 339 TTATIGGNNIVPVTPPLGLRACYLFALFGAPIALITIGDLGKFLSECTIWLYKHMRRGSA 398 Qy 191 KVEDTFIKW-----NVSQKIRIISTIIFILFGCV 220
Query Match 13.0%; Score 273; DB 2; Length 392; Best Local Similarity 25.5%; Pred. No. 1..8e-14; Matches 83; Conservative 66; Mismatches 106; Indels 76; Gaps 13;	Db 399 RLDSSAWKRFRGLEDSISDDLESASRNQDSSILDMMDMIEDKSEPVLMVFTII----L 452 Qy 221 LIFVALPAITFKHIGWSALDAYFVVITLTIGFDYAGGSDEIYLDFYKPVWFWLIV 280 Db 453 LYAFGGILFSLEDWSYMAFVYSFSPLSLTIGFDIVPENHD----YIAIMLIYUGV 506 Qy 281 GLAYFAAVLISMIG-----DWLRVISKTKT-----EEVGEFRAH 313 Db 507 GLSVTTMCIDLAQIYIQKIHYFGRKFGQGTLQYLICKRMILERLAMGQGEETLRKYH 566
Qy 5.8 LIIGATVPKALEOPHEISORTTIVIQKOTFISOS-----CVNSTELDELQOQ-V 107 Db 11.8 -----PSRIEPILE-----KIERDAYDQNQWDFRLIQLDISEIDFLFLNTR 163 Qy 108 AAINAGIPLGNTSNQISHWDLGSSPFPAFYTITIGFGNISPRTEGGKIFCITYALLGI 167 Db 164 AALNGIMWDRNLTS-----BNWTFQOAFFAGTLLSTVGYGRVSRTYEGRKLFTLYCIGI 221	Qy 314 AAEWTANTVAEKFETRRLSVEIYDK 339 Db 567 AVE-----KFEREQEQLQQRMEE 585
Qy 168 PLEGFLLGKV-----GDOLGTIGKGIAKVEDPIKNNVSQTKIRIISTI 212 Db 222 PLTALLSAIVARMREPPSHKLRLGHLNQNOLIGHF-----TVNHIQOLIHVG 265	RESULT 13 T15584 hypothetical protein C24A3.6 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999 C;Accession: T15584 R;Favallio, T. submitted to the EMBL Data Library, November 1995 A;Description: The sequence of C. elegans cosmid C24A3. A;Accession: T15584 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-325 <FAV> A;Cross-references: EMBL:040424; PID:91065542; PID:AAA81455.1; CBSP:CC24A C;Genetics: A;Gene: CESP:C24A3.6 A;Introns: 21/1; 63/3; 131/1; 193/3; 206/3
Qy 21.3 IFILFGCVLFV-ALPAITFKHIGWSALDAYFVVITLTIGFDYAGGS-DIEYLD 269 Db 266 V-VFASLILFVFPAFPWVSSITDWSLDAFVYCFCVSLTTLGDFPQDDENQSPRGL 324 Qy 270 YKEPVVWFVILVGLAYFAAVLISMIGD 294 Db 325 YKIGATVYLMGGLCMMIFLATIYD 349	Query Match 12.8%; Score 269; DB 2; Length 325; Best Local Similarity 25.1%; Pred. No. 3..1e-14; Matches 86; Conservative 53; Mismatches 88; Indels 116; Gaps 11; Qy 46 TVSTYF-----LWVVLVLYIIGATVFKALEQPHBISQRTTIVQKOTFISQHSCVN 95 Db 10 TILTFTQKTFPKGLPLLILVAVTLLGAWIFWMIGENE-----REMLIEQQK--- 56 Qy 96 STELDLQIQIVAAIN-----AGLIPLGNTSNQIS 125 Db 57 -ERDELRRTYKINOLQIKQRQLNTAERYNRTAKVLTTFQETIGIVPA--DMDRD 112 Qy 126 HDLGGSSFFPACTVITIGFGNISPRTEGGKIFCIVYALLGIPFGFLLAGVQDQLSTIF 185 Db 113 HWTFLGSIFYCMVTTTIGYGNIVPCTGWGRPATILYAFIPIPLTVLSY----CLGSLP 168 Qy 186 GKIGIAKYBDFTIKWNYSQTKIRIIS----- Db 169 AKGCKMLWRFLIK-----STRVSKDLSNKISEADNIEGTTAIPSAEKTEENNDD 222 Qy 211 ---TIIIFILFGCVLFVALPAITFKHIGWSALDAIYFVVITLTIGFDYAGGSDEIYLV 267 Db 223 LSFPISGHLITVWIFCAVLFPTFLBEWDFCTSLYFISPTTIGFDILP--SDYDFM 280 Qy 268 DFIKPVWFWFILVGLAYFAAVLISMIGDWLRVTS-----KKCTKE 305 Db 281 ----PIVGVLLLJGSLSVSTWNTLIOQQIBALASVRRKCK 319
RESULT 12 H88124 protein T12C9.3 [imported] - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Accession: H88124 R;anonymous, The C. elegans Sequencing Consortium. A;Title: Genome sequence of the nematode <i>C. elegans</i> , a platform for investigating biology Science 282, 2012-2018, 1998 A;Reference number: AT5000; MURID:99069613; PMID:9851916 A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_elegans/ A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Accession: H88124 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-1910 <SO> A;Cross-references: GB:chr_II; PIDN:AC71141.1; PID:91086770; GSPDB:GN00020; CESP:T12C9.3 A;Note: proline-rich C;Genetics: A;Gene: T12C9.3 A;Map position: 2	Query Match 13.0%; Score 273; DB 2; Length 1910; Best Local Similarity 23.3%; Pred. No. 1..2e-13; Matches 104; Conservative 74; Mismatches 122; Indels 146; Gaps 18; Qy 18 PRISL-PSTKPTYLAS-RVESDTTI--NMVKMKVTSTIPLVVV----LYLIGATVKA 67 Db 162 PQFSRRFLFPGILESARPDDETTTLQNRKYAKLALPHIVVVCVYATIGANFYT 221 Qy 68 LEOPHE----ISORTTIVQKOTFISCVNSTELO-----ELI-----Q 104 Db 222 LESPNEDLKETCRKTIAEMRSNLYK--INNNEKWTWEDIEKELMLYSEKLYKAFKE 278 Qy 105 QIVAAATNGGIPL-----GNTSNQISH-----WDLGSSFFPAG 137 Db 279 QTVRYSDRTTIGEGRSSYYEADETGEBSERGRHRGKNDRGSPKMWTTSSAIFFAA 338 Qy 138 TTITIGGNNISPRTEGGKIFCITYALLGIPLFGFLLAGVQDQLG-TIF----GKGIA 190
	RESULT 14 T24265 hypothetical protein T01B.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C;Accession: T24265

R; Wilkinson, J.	Submitted to the EMBL Data Library, March 1996	Matches 81;	Conservative 50;	Mismatches 121;	Indels 32;	Gaps 7;
A; Reference number: Z19866		Qy 42 MKWRTISTI-----FLVWVLYLIGATVPALE----QPHEISQRTTIVIQKOTFIS 89				
A; Accession: T24265		Db 36 MKFRNVLRLIAALGHIALYCFVUCYVFGAGAWYFHOLEGENETELHDKOREYAMNLKDVIAK 95				
A; Status: preliminary; translated from GB/EMBL/DDJB						
A; Molecule type: DNA		Qy 90 QHSCVNSTELDELQGQVAATINAGITPLGN-----TSNQISHWDLGSSPPFGATVTT 142				
A; Residues: 1-122 <WIL>		Db 96 LATTEVAEINEHLMFLRNTLHSIDENLYLIFNEPTQ1YPKRWTPSSULEFSFTLT 155				
A; Cross-references: UNIPROT:Q22042; EMBL:Z70036; PIDN:CAA93875.1; GSPDB:GN00028; CESP:TC		Qy 143 IGFHNISPRTEGGKFCITYALLGIPLGFGELLAGVGDOGLCTIFGKGIAKYEDTFIKWNVS 202				
C; Genetics:		Db 156 IGYGNVTPHTOQCCKYFLMIYGAFLPLFLTIADGGRFSKTAIMALVQKVSKRELKQSD 215				
A; Gene: CESP:T01B4.1						
A; Map position: X						
A; Introns: 95/3; 142/1; 224/3; 290/1; 458/1						
Query Match Score 12.7%; Best Local Similarity 23.1%; Matches 99; Conservative 64; Mismatches 132; Indels 134; Gaps 15;		Qy 203 QTKIRLISTI--ITFLFGCULFEVALPALEFKHIGW---SALDAIYFVWITLTIGFG 255				
Db 50 IFLVVVLYLIGATVPALEOPHE-----ISQRTTIVIQKOTFISQHSCVNSTE 98		Db 216 EHLREIAEVSPYLVLVLAGLFVVFIAIGSAVPLWENOLTYFDSVYFSYMSLTTIGLG 275				
Qy 41 LILIGYACAGGMMQALETDQQQLEEAERKVRVLSSESSLAVNLLEHKQANCGSNE 100		Qy 256 DYAGGSDIEYLDFKKPVWWFILVNGLAYPAVLSMIGDWLRV 299				
Db 99 LDELIQVVAAINAGITPLGENTS-NQISHWDLGSSPFAGTVTTTGFGNISPRTEGGKI 157		Db 276 DIVP----PRMDFELPTL-IYITIGLMLTTAELQADYFLRY 313				
Db 101 -----KCRLHDTKTFQRSDERGEWRWDENWSVSFATIIFTKJACKNLGRI 155						
Qy 158 FCIIYALGIDFLFGFLAGVGD-----QLGTLFGKG 188						
Db 156 ATIYGMIGIPLMLFYVLKNFGELCVKWKAKIQFNQYQCLKXCFGRKQKRASSLASTSKE 215						
Qy 189 IAKV-----EDTF--IKWNVSQTKIRLISTIIFLFCVLFVALPALEFKLEGWS 237						
Db 216 MLEVFFPEVPPDKEDTFQLRNG-----LLVIVLFVLCFPVGSWEWND 260						
Qy 238 ALDAYFVVTIITTGDDYAGGSDEIYLDFYKPVWFWIL-VGLAYFAAVLSMIGD- 294						
Db 261 FLTAFYFFVVSITGDIYV-----DPRTACALFVLYFIGLAFMAYVALLQER 312						
Qy 295 -----W-LRVISKTKTKEVEGFERHAEEWTANV----- 322						
Db 313 VENQMVWALELIDQKYEQKLKDMDYDEKADKNDMHFSKKEPYVRGPRLQDLRGPD 372						
Qy 323 AEFKEPTRRLS-----VLIYDKFQFATSIKRLSSEL----AGNNHQELTPCERTLS 370						
Db 373 LKISGGRSSSSDASSVITEASDEDTHFKVGRALAEAFDERSNHGTQINSCT---- 428						
Qy 371 VNHLTNERD 379						
Db 429 ---VSNEHD 434						
RESULT 15						
T21118						
hypothetical protein F19D8.1 - Caenorhabditis elegans						
C; Species: Caenorhabditis elegans						
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004						
C; Accession: T21118						
R; Swinburne, J.; Ainscough, R.						
Submitted to the EMBL Data Library, August 1996						
A; Reference number: Z19377						
A; Accession: T21118						
A; Status: preliminary; translated from GB/EMBL/DDJB						
A; Molecule type: DNA						
A; Residues: 1-452 <WIL>						
A; Cross-references: UNIPROT:Q93531; EMBL:Z78541; PIDN:CAR01740.1; GSPDB:GN00028; CESP:P1						
C; Genetics:						
A; Gene: CESP:F19D8.1						
A; Map Position: X						
A; Introns: 31/1; 82/2; 101/3; 157/1; 197/1; 230/3; 267/2; 325/3; 356/1; 404/3						
Query Match Score 12.5%; Best Local Similarity 28.5%; Pred. No. 1.7e-13;						

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 13, 2005, 08:40:02 ; Search time 90.2442 Seconds  
(without alignments)

Scoring table: BLOSUM62

Title: US-09-503-089A-2  
Perfect score: 2100

Sequence: 1 MAAPDILDPKSAANQSKPRL.....LNGLTPHAGEEIAVNIK 411.

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1726220 seqs, 316332138 residues

Total number of hits satisfying chosen parameters: 1726220

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA:  
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 2: /cggn2\_6/\_ptodata/1/pubaa/PCTR\_NEW\_PUB.pep;\*  
 3: /cggn2\_6/\_ptodata/1/pubaa/US06\_NEW\_PUB.pep;\*  
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RESULT 1  
US-09-892-360-18  
; Sequence 18, Application US/09892360  
; Publication No. US20040101833A1  
; GENERAL INFORMATION:  
; APPLICANT: LAZDUNSKI, MICHEL  
; ATTORNEY: LESAGE, FLORIAN  
; APPLICANT: ROMEY, GEORGES  
; TITLE OF INVENTION: HUMAN TREK2, A STRETCH-AND ARACHIDONIC ACID-SENSITIVE  
; TITLE OF INVENTION: K+ CHANNEL ACTIVATED BY INHALATIONAL ANESTHETICS AND  
; TITLE OF INVENTION: RILUZOLE  
; FILE REFERENCE: 1256-R-00  
; CURRENT APPLICATION NUMBER: US/09892360  
; CURRENT FILING DATE: 2001-06-27  
; PRIOR APPLICATION NUMBER: 60/214,559  
; PRIOR FILING DATE: 2000-06-27  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 411  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; US-09-892-360-18

Query Match Score Description

Result No.	Score	Match	Length	DB ID	Description
1	2100	100.0	411	11 US-09-892-360-18	Sequence 18, Appl
2	2095	99.8	411	11 US-09-892-360-18	Sequence 2, Appl
3	2095	99.8	411	14 US-10-121-746-2	Sequence 83, Appl
4	2095	99.8	411	16 US-10-745-210-2	Sequence 2, Appl
5	2095	99.8	411	16 US-10-349-528-31	Sequence 31, Appl
6	2095	99.8	411	17 US-10-916-644-83	Sequence 83, Appl
7	2095	99.8	411	17 US-10-916-644-83	Sequence 83, Appl
8	2089	99.5	422	16 US-10-528-20	Sequence 20, Appl
9	2062	98.2	426	8 US-08-816-011-45	Sequence 45, Appl
10	2062	98.2	426	17 US-10-870-49-45	Sequence 45, Appl
11	2058	98.0	426	17 US-10-870-492-57	Sequence 57, Appl

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	2100	100.0	411	11 US-09-892-360-18	Sequence 18, Appl
2	2095	99.8	411	11 US-09-892-360-18	Sequence 2, Appl
3	2095	99.8	411	14 US-10-121-746-2	Sequence 83, Appl
4	2095	99.8	411	16 US-10-745-210-2	Sequence 2, Appl
5	2095	99.8	411	16 US-10-349-528-31	Sequence 31, Appl
6	2095	99.8	411	17 US-10-916-644-83	Sequence 83, Appl
7	2095	99.8	411	17 US-10-916-644-83	Sequence 83, Appl
8	2089	99.5	422	16 US-10-528-20	Sequence 20, Appl
9	2062	98.2	426	8 US-08-816-011-45	Sequence 45, Appl
10	2062	98.2	426	17 US-10-870-49-45	Sequence 45, Appl
11	2058	98.0	426	17 US-10-870-492-57	Sequence 57, Appl

Sequence 58, Appl  
Sequence 60, Appl  
Sequence 59, Appl  
Sequence 6, Appl  
Sequence 8, Appl  
Sequence 5, Appl  
Sequence 4, Appl  
Sequence 4, Appl  
Sequence 2, Appl  
Sequence 46, Appl  
Sequence 2, Appl  
Sequence 73, Appl  
Sequence 2, Appl  
Sequence 106, Appl  
Sequence 2, Appl  
Sequence 10, Appl  
Sequence 55, Appl  
Sequence 12, Appl  
Sequence 65, Appl  
Sequence 44, Appl  
Sequence 29, Appl  
Sequence 8, Appl  
Sequence 19, Appl  
Sequence 15, Appl  
Sequence 12, Appl  
Sequence 66, Appl  
Sequence 64, Appl  
Sequence 29, Appl  
Sequence 29, Appl  
Sequence 19, Appl  
Sequence 19, Appl  
Sequence 6, Appl  
Sequence 60, Appl

ALIGMENTS

RESULT 2  
 US-09-828-746-2  
 ; Sequence 2, Application US/09828746  
 ; Patent No. US2002028485A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Helen Jane Meadows  
 ; APPLICANT: Conrad Gerald Chapman  
 ; TITLE OF INVENTION: NOVEL COMPOUNDS  
 ; FILE REFERENCE: GP-30031-D1  
 ; CURRENT APPLICATION NUMBER: US/09/828-746  
 ; CURRENT FILING DATE: 2001-04-09  
 ; PRIOR APPLICATION NUMBER: US 09/236,080  
 ; PRIOR FILING DATE: 1999-01-25  
 ; PRIOR APPLICATION NUMBER: EP 98300570-3  
 ; PRIOR FILING DATE: 1998-01-27  
 ; PRIOR APPLICATION NUMBER: UK 9822135-1  
 ; PRIOR FILING DATE: 1998-10-09  
 ; NUMBER OF SEQ ID NOS: 6  
 ; SOFTWARE: FastSEQ for Windows Version 3.0  
 ; SEQ ID NO: 2  
 ; TYPE: PRT  
 ; ORGANISM: HOMO SAPIENS  
 US-09-828-746-2

Query Match 99.8%; Score 2095; DB 9; Length 411;  
 Best Local Similarity 99.8%; Pred. No. 1.1e-187;  
 Matches 410; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 61 GATVFKALEQPHISORTTIVQKQTFSQHSCVNSTELDELQIVAAINGIPLGNT 120  
 Qy 121 SNOISHMDLGSSFFACTVTITIGFGNISPRTEGGKLFCITYYALGIPLFSPFLLAGVGDQ 180  
 Db 121 SNOISHMDLGSSFFACTVTITIGFGNISPRTEGGKLFCITYYALGIPLFSPFLLAGVGDQ 180  
 Qy 121 SNOISHMDLGSSFFACTVTITIGFGNISPRTEGGKLFCITYYALGIPLFSPFLLAGVGDQ 180  
 Db 121 SNOISHMDLGSSFFACTVTITIGFGNISPRTEGGKLFCITYYALGIPLFSPFLLAGVGDQ 180  
 Qy 61 GATVFKALEQPHISORTTIVQKQTFSQHSCVNSTELDELQIVAAINGIPLGNT 120  
 Db 61 GATVFKALEQPHISORTTIVQKQTFSQHSCVNSTELDELQIVAAINGIPLGNT 120  
 Qy 1 MAAPDLDPKSAAQNSKERLSFSTKPTVLASRVEDTTINMKWCVTSTIFLVVLYLI 60  
 Db 1 MAAPDLDPKSAAQNSKERLSFSTKPTVLASRVEDTTINMKWCVTSTIFLVVLYLI 60  
 Qy 61 GATVFKALEQPHISORTTIVQKQTFSQHSCVNSTELDELQIVAAINGIPLGNT 120  
 Db 61 GATVFKALEQPHISORTTIVQKQTFSQHSCVNSTELDELQIVAAINGIPLGNT 120  
 Qy 121 SNOISHMDLGSSFFACTVTITIGFGNISPRTEGGKLFCITYYALGIPLFSPFLLAGVGDQ 180  
 Db 121 SNOISHMDLGSSFFACTVTITIGFGNISPRTEGGKLFCITYYALGIPLFSPFLLAGVGDQ 180  
 Qy 121 SNOISHMDLGSSFFACTVTITIGFGNISPRTEGGKLFCITYYALGIPLFSPFLLAGVGDQ 180  
 Db 121 SNOISHMDLGSSFFACTVTITIGFGNISPRTEGGKLFCITYYALGIPLFSPFLLAGVGDQ 180  
 Qy 161 LGTIFGKCIAKYEDTFIKWNVSOTKIRIISTIFLPGCVLFLVALPAIIFHGEGMSALD 240  
 Db 161 LGTIFGKCIAKYEDTFIKWNVSOTKIRIISTIFLPGCVLFLVALPAIIFHGEGMSALD 240  
 Qy 121 AIFYVVITLTIGFDYAGGS DIEYLDFYKPVWMFLVGLAYFAAVLSMIGDWLRVIS 300  
 Db 121 AIFYVVITLTIGFDYAGGS DIEYLDFYKPVWMFLVGLAYFAAVLSMIGDWLRVIS 300  
 Qy 241 AIFYVVITLTIGFDYAGGS DIEYLDFYKPVWMFLVGLAYFAAVLSMIGDWLRVIS 300  
 Db 241 AIFYVVITLTIGFDYAGGS DIEYLDFYKPVWMFLVGLAYFAAVLSMIGDWLRVIS 300  
 Qy 301 KKTKEEVGEFRAAENTVATAEKFTRRLSVEYDKFORATSIKRKLSAELAGHNQ 360  
 Db 301 KKTKEEVGEFRAAENTVATAEKFTRRLSVEYDKFORATSIKRKLSAELAGHNQ 360  
 Qy 361 ELTPCRTLTSYNHNLNERDVLPLKTESITYLGLTPHCAGEEIAVENIK 411  
 Db 361 ELTPCRTLTSYNHNLNERDVLPLKTESITYLGLTPHCAGEEIAVENIK 411  
 Qy 361 ELTPCRTLTSYNHNLNERDVLPLKTESITYLGLTPHCAGEEIAVENIK 411  
 Db 361 ELTPCRTLTSYNHNLNERDVLPLKTESITYLGLTPHCAGEEIAVENIK 411  
 RESULT 4  
 US-10-745-210-2

Sequence 2, Application US/10745210  
; Publication No. US20040143855A1  
; GENERAL INFORMATION:  
; APPLICANT: TONONI, Giulio  
; TITLE OF INVENTION: ION CHANNELS AS TARGETS FOR SLEEP-RELATED DRUGS  
; FILE REFERENCE: 05440.0-0044  
; CURRENT APPLICATION NUMBER: US/10/745,210  
; CURRENT FILING DATE: 2003-12-23  
; PRIOR APPLICATION NUMBER: US 60/436,201  
; PRIOR FILING DATE: 2001-12-23  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO: 2  
; LENGTH: 411  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-745-210-2

Query Match 99.8%; Score 2095; DB 16; Length 411;  
Best Local Similarity 99.8%; Pred. No. 1.1e-187;  
Matches 410; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAAPDLDPKSAQNSKPRLSSTKPTVLASRVEDDTINVMKKTSTIFLVVLYLII 60  
Db 1 MAAPDLDPKSAQNSKPRLSSTKPTVLASRVEDDTINVMKKTSTIFLVVLYLII 60

Qy 61 GATVFKALEQPHEISQRTTIVIQQTFSQHSCVNSTELDELQIQVAIAINAGIPLGNT 120  
Db 61 GATVFKALEQPHEISQRTTIVIQQTFSQHSCVNSTELDELQIQVAIAINAGIPLGNT 120

Qy 121 SNOQISHWDLGSSPFAGTYITIGFGNISPRTEGGKICFIIYALGIPLFGEFLAGVSDQ 180  
Db 121 SNOQISHWDLGSSPFAGTYITIGFGNISPRTEGGKICFIIYALGIPLFGEFLAGVSDQ 180

Qy 181 LGTFPGKGIAKVEDFTIKNVSQTKIRISTIIFLGCVLFAALPAIFKIEGWSALD 240  
Db 181 LGTFPGKGIAKVEDFTIKNVSQTKIRISTIIFLGCVLFAALPAIFKIEGWSALD 240

Qy 241 AIVFVITLTIGFGDYAGGSDEYLDFYKPVWFWLVLGLAYFAAVLSMIGWLRYIS 300  
Db 241 AIVFVITLTIGFGDYAGGSDEYLDFYKPVWFWLVLGLAYFAAVLSMIGWLRYIS 300

Qy 301 KKTKEEVGFRAAENTANVTAEFKETRRLSVEIYDKFORATSIKRKLSAELAGHNQ 360  
Db 301 KKTKEEVGFRAAENTANVTAEFKETRRLSVEIYDKFORATSIKRKLSAELAGHNQ 360

Qy 361 ELTPCRRTLSVNHLTNERDVLPPLKTESIYNGLPHCAEGEAVIENIK 411  
Db 361 ELTPCRRTLSVNHLTSERDVLPPLKTESIYNGLPHCAEGEAVIENIK 411

RESULT 6  
US-10-976-644-83  
; Sequence 83, Application US/10976644  
; Publication No. US20050112662A1  
; GENERAL INFORMATION:  
; APPLICANT: Miller, Andrew P.  
; APPLICANT: Curran, Mark Edward  
; APPLICANT: Hu, Ping  
; APPLICANT: Rutter, Marc  
; APPLICANT: Wang, Jian-Wang  
; TITLE OF INVENTION: Novel Human Potassium Channel 1.8  
; FILE REFERENCE: SEQ-15P  
; CURRENT APPLICATION NUMBER: US/10/976,644  
; CURRENT FILING DATE: 2004-10-29  
; PRIOR APPLICATION NUMBER: US/09/336,643  
; PRIOR FILING DATE: 1999-06-18  
; PRIOR APPLICATION NUMBER: 60/076,687  
; PRIOR FILING DATE: 1998-08-07  
; PRIOR APPLICATION NUMBER: 60/116,448  
; PRIOR FILING DATE: 1999-01-19  
; PRIOR APPLICATION NUMBER: PCT/US99/03826  
; PRIOR FILING DATE: 1999-02-22  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO: 83  
; LENGTH: 411  
; TYPE: PRT  
; ORGANISM: H. sapiens  
US-10-976-644-83

Query Match 99.8%; Score 2095; DB 17; Length 411;  
Best Local Similarity 99.8%; Pred. No. 1.1e-187;  
Matches 410; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAAPDLDPKSAQNSKPRLSSTKPTVLASRVEDDTINVMKKTSTIFLVVLYLII 60  
Db 1 MAAPDLDPKSAQNSKPRLSSTKPTVLASRVEDDTINVMKKTSTIFLVVLYLII 60

Qy 61 GATVFKALEQPHEISQRTTIVIQQTFSQHSCVNSTELDELQIQVAIAINAGIPLGNT 120

241 AIYFWVITLTIGFDDYVAGGSIDIEYDVKPWWFVWLVGLAYFAAVLSMIGDWLRVIS 3 00  
61 GATVFKALEQPHESIQRRTIVIQKOTFISQHSCVNSTELDELIOQVAAINAGIPLGNT 120  
Db Qy 121 SNOQSHWLGSFFPAGTVTTIGRGNISPRTEGGKIFCITYALIGIPFGFLLAGVGQ 180  
Db Qy 121 SNOQSHWLGSFFPAGTVTTIGRGNISPRTEGGKIFCITYALIGIPFGFLLAGVGQ 180  
Db Qy 181 LGTIFGKGIAKVEDFTKVNVSQTKRRIISTIIFLFGCYLFVALPAIKFHLEGWSALD 240  
Db Qy 181 LGTIFGKGIAKVEDFTKVNVSQTKRRIISTIIFLFGCYLFVALPAIKFHLEGWSALD 240  
Db Qy 241 AIYFWVITLTIGFDDYVAGGSIDIEYDVKPWWFVWLVGLAYFAAVLSMIGDWLRVIS 300  
Db Qy 241 AIYFWVITLTIGFDDYVAGGSIDIEYDVKPWWFVWLVGLAYFAAVLSMIGDWLRVIS 300  
Db Qy 301 KKTKEEVGEFRAAETWTANVTAAEKFETRRRLSVEIYDKFQRTSIKRKLSAELAGNHQ 3 60  
Db Qy 301 KKTKEEVGEFRAAETWTANVTAAEKFETRRRLSVEIYDKFQRTSIKRKLSAELAGNHQ 3 60  
Db Qy 361 ELTPCRRTLSVNLHTNERDVLPLKTESTYLNGLTPHCAGEIAVIENIK 4 11  
Db Qy 361 ELTPCRRTLSVNLHTNERDVLPLKTESTYLNGLTPHCAGEIAVIENIK 4 11  
Db Qy 361 ELTPCRRTLSVNLHTSERDVLPPLKTESTYLNGLTPHCAGEIAVIENIK 4 11  
Db Qy 361 ELTPCRRTLSVNLHTSERDVLPPLKTESTYLNGLTPHCAGEIAVIENIK 4 11  
Db Qy RESULT 8  
Db Qy US-10-349-528-20  
Db Qy ; Sequence 20, Application US/10349528  
Db Qy ; Publication No. US20040255668A1  
Db Qy ; GENERAL INFORMATION:  
Db Qy ; APPLICANT: RAMANATHAN, Chandra  
Db Qy ; APPLICANT: GOPAL, Shuba  
Db Qy ; APPLICANT: MINTIER, Gabe  
Db Qy ; APPLICANT: FEDER, John  
Db Qy ; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR (GPCR) VARIANTS AND METHODS OF  
Db Qy ; TITLE OF INVENTION: USE THEREOF  
Db Qy ; FILE REFERENCE: D0210  
Db Qy ; CURRENT APPLICATION NUMBER: US/10/349,528  
Db Qy ; CURRENT FILING DATE: 2003-01-22  
Db Qy ; NUMBER OF SEQ ID NOS: 35  
Db Qy ; SOFTWARE: PatentIn version 3.2  
Db Qy ; SEQ ID NO: 20  
Db Qy ; LENGTH: 422  
Db Qy ; TYPE: PRT  
Db Qy ; ORGANISM: HOMO SAPIENS  
Db Qy US-10-349-528-20  
Db Qy Query Match 99.5%; Score 2089; DB 16; Length 422;  
Db Qy Best Local Similarity 99.3%; Pred. No. 4.1e-187; 0; Indels 0; Gaps 0;  
Db Qy Matches 408; Conservative 3; Mismatches 0;  
Db Qy 1 MAAPDLDPKSAAQNSKPRLSFSKTPVLAARSVESTDINVMKWKTVSTIFLYVYLII 60  
Db Qy 12 LAAPDLDPKSAAQNSKPRLSFSKTPVLAARSVESTDINVMKWKTVSTIFLYVYLII 71  
Db Qy 61 GATVPKALEQPHESIQRRTIVIQKOTFISOHSCVNSTELDELIOQVAAINAGIPLGNT 120  
Db Qy 72 GATVPKALEQPHESIQRRTIVIQKOTFISOHSCVNSTELDELIOQVAAINAGIPLGNT 131  
Db Qy 121 SNOQSHWLGSFFPAGTVTTIGRGNISPRTEGGKIFCITYALIGIPFGFLLAGVGQ 180  
Db Qy 132 SNOQSHWLGSFFPAGTVTTIGRGNISPRTEGGKIFCITYALIGIPFGFLLAGVGQ 191  
Db Qy 181 LGTIFGKGIAKVEDFTKVNVSQTKRRIISTIIFLFGCYLFVALPAIKFHLEGWSALD 240  
Db Qy 192 LGTIFGKGIAKVEDFTKVNVSQTKRRIISTIIFLFGCYLFVALPAIKFHLEGWSALD 251  
Db Qy 241 AIYFWVITLTIGFDDYVAGGSIDIEYDVKPWWFVWLVGLAYFAAVLSMIGDWLRVIS 3 00  
Db Qy 252 AIYFWVITLTIGFDDYVAGGSIDIEYDVKPWWFVWLVGLAYFAAVLSMIGDWLRVIS 3 11  
Db Qy 61 GATVFKALEQPHESIQRRTIVIQKOTFISOHSCVNSTELDELIOQVAAINAGIPLGNT 120  
Db Qy 61 GATVFKALEQPHESIQRRTIVIQKOTFISQHSCVNSTELDELIOQVAAINAGIPLGNT 120  
Db Qy 121 SNOQSHWLGSFFPAGTVTTIGRGNISPRTEGGKIFCITYALIGIPFGFLLAGVGQ 180  
Db Qy 121 SNOQSHWLGSFFPAGTVTTIGRGNISPRTEGGKIFCITYALIGIPFGFLLAGVGQ 180  
Db Qy 181 LGTIFGKGIAKVEDFTKVNVSQTKRRIISTIIFLFGCYLFVALPAIKFHLEGWSALD 240  
Db Qy 181 LGTIFGKGIAKVEDFTKVNVSQTKRRIISTIIFLFGCYLFVALPAIKFHLEGWSALD 240  
Db Qy RESULT 9  
Db Qy US-08-816-011-45  
Db Qy ; Sequence 45, Application US/08816011  
Db Qy ; Publication No. US20030165806A1

GENERAL INFORMATION:  
 APPLICANT: Price, Laura A.  
 APPLICANT: Pausch, Mark H.  
 TITLE OF INVENTION: Potassium Channels, Nucleotide Sequences Encoding Them, and Methods of Using Same  
 NUMBER OF SEQUENCES: 56  
 ADDRESS: American Home Products Corporation  
 STREET: One Campus Drive  
 CITY: Parsippany  
 STATE: New Jersey  
 COUNTRY: USA  
 ZIP: 07054  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/816,011  
 FILING DATE: 11-MAR-1997  
 CLASSIFICATION: 536  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Matthews, Gale F.  
 REFERENCE/DOCKET NUMBER: 32, 269  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201-683-2134  
 TELEFAX: 201-683-4117  
 INFORMATION FOR SEQ ID NO: 45:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 426 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-816-011-45

Query Match 98.2%; Score 2062; DB 8; Length 426;  
 Best Local Similarity 98.5%; Pred. No. 1.4e-18;  
 Matches 405; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 US-10-870-492-45

Query Match 98.2%; Score 2062; DB 17; Length 426;  
 Best Local Similarity 98.5%; Pred. No. 1.4e-18;  
 Matches 405; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 US-10-870-492-45

Qy 1 MAAPDLDPKSAAQNSKPRLSFSTKPTVLASRVSDEDTINMKWKTSTIFLVVLYLII 60  
 Db 16 VAAPDLDPKSAAQNSKPRLSFSTKPTVLASRVSDEDTINMKWKTSTIFLVVLYLII 75

Qy 61 GATVKALEQPHISQRRTIVIQQTFSQHSCVNSTELDIQIVAAINAGIPLGNT 120  
 Db 76 GATVKALEQPHISQRRTIVIQQTFSQHSCVNSTELDIQIVAAINAGIPLGNT 135

Qy 121 SNOQSHWLGLSSPFAGSTVITIGFGNTSPTEGGKIFCIIYALLGIPLGFLGFLAGVSDQ 180  
 Db 136 SNOQSHWLGLSSPFAGSTVITIGFGNTSPTEGGKIFCIIYALLGIPLGFLGFLAGVSDQ 195

Qy 181 LGTFGKGIAKVEDTFLKWNVSOTKIRLSTITIPLFKHIEGWSALD 240  
 Db 196 LGTFGKGIAKVEDTFLKWNVSOTKIRLSTITIPLFKHIEGWSALD 255

Qy 241 AIVPPVITLTIGFGDVYAGSDIEYLDFYKPVWFWILVGLAYFAAVLSMIGDWLRVIS 300  
 Db 256 AIVPPVITLTIGFGDVYAGSDIEYLDFYKPVWFWILVGLAYFAAVLSMIGDWLRVIS 315

Qy 301 KCTKEEYGFRAAENTVTAEFKETRRLSVEIYDKFORATSIKRKLSAELAGHNQ 360  
 Db 316 KCTKEEYGFRAAENTVTAEFKETRRLSVEIYDKFORATSIKRKLSAELAGHNQ 375

Qy 361 ELTPCRTLTSVNHLTNERDVLPLPLKTESIYINGLTPHCAGERIAVENIK 411  
 Db 376 ELTPCRTLTSVNHLTSERDVLPLPLKTESIYINGLAPCAGEIAVENIK 426

RESULT 11  
 US-10-870-492-57

Sequence 57, Application US/10870492

GENERAL INFORMATION:  
 APPLICANT: Pausch, Mark H.  
 TITLE OF INVENTION: Potassium Channels, Nucleotide Sequences Encoding Them,  
 FILE REFERENCE: 01142.014 SEQUENCE LISTING  
 CURRENT APPLICATION NUMBER: US/10/870,492  
 CURRENT FILING DATE: 2004-06-18  
 PRIOR APPLICATION NUMBER: US/09/503,849  
 PRIOR FILING DATE: 2000-02-15  
 PRIOR APPLICATION NUMBER: 08/816,011  
 PRIOR FILING DATE: 1997-03-11  
 PRIOR APPLICATION NUMBER: PCT/US95/14364

RESULT 10  
 US-10-870-492-45  
 Sequence 45, Application US/10870492

PRIOR FILING DATE: 1995-10-25  
 PRIOR APPLICATION NUMBER: 07/332,312  
 PRIORITY NUMBER: 07/332,312  
 NUMBER OF SEQ ID NOS: 74  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO: 57  
 LENGTH: 426  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-870-492-57

Query Match 98.0%; Score 2058; DB 17; Length 426;  
 Best Local Similarity 98.3%; Pred. No. 3, 4e-184;  
 Matches 404; Conservative 3; Mismatches 0;  
 Indels 0; Gaps 0;

Qy 1 MAAPDILDPKSAQNSKPKLPSFKPTVLAQVSEDTINTMKWKTIVSTIFLVVLYLII 60  
 Db 16 VAAPDILDPKSAQNSKPKLPSFKPTVLAQVSEDTINTMKWKTIVSTIFLVVLYLII 75

Qy 61 GATVFKALEQPKHEISORTTIVQKPFISQHSCVNSTELDELIQVVAANAGIPIGNT 120  
 Db 76 GATVFKALEQPKHEISORTTIVQKPFISQHSCVNSTELDELIQVVAANAGIPIGNT 135

Qy 121 SNOQISHWDLGSSFFAGTVTTGGGNISPTEGGKFCIYALGIPFGPLLAGVGQDQ 180  
 Db 136 SNOQISHWDLGSSFFAGTVTTGGGNISPTEGGKFCIYALGIPFGPLLAGVGQDQ 195

Qy 181 LGTIFGKGIARVEDTFIKWNVSQTQKRLISTIIFLPGCULFVALPAIIFKHEGMSALD 240  
 Db 196 LGTIFGKGIARVEDTFIKWNVSQTQKRLISTIIFLPGCULFVALPAIIFKHEGMSALD 255

Qy 241 AIYFVVTITLTGFGDYVAGGSDEIYLDFYKPVWWFILVGLAYFAVLSMIGDWLRVIS 300  
 Db 256 AIYFVVTITLTGFGDYVAGGSDEIYLDFYKPVWWFILVGLAYFAVLSMIGDWLRVIS 315

Qy 301 KKTKEEVGEFRAAENTVTAEFKTRRLSVEYDKFQRATSIKRKLSAELAGNHQ 360  
 Db 316 KKTKEEVGEFRAAENTVTAEFKTRRLSVEYDKFQRATSIKRKLSAELAGNHQ 375

Qy 361 ELTPCRTLTSVNLHTNEDVLPPLKTESVYLTPHAGEEIAVENIK 411  
 Db 376 ELTPCRTLTSVNLHTNEDVLPPLKTESVYLTPHAGEEIAVENIK 426

RESULT 1.3  
 US-10-870-492-60  
 Sequence 60, Application US/10870492  
 Publication No. US2005032165A1

GENERAL INFORMATION:  
 APPLICANT: PAUSCH, MARK H.  
 TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,  
 AND METHODS OF USING SAME  
 FILE REFERENCE: 01142..0114 SEQUENCE LISTING  
 CURRENT APPLICATION NUMBER: US/10-870-492  
 PRIOR APPLICATION NUMBER: US/09/503 , 849  
 PRIOR FILING DATE: 2000-02-15  
 PRIOR APPLICATION NUMBER: 08/816,011  
 PRIOR FILING DATE: 1997-03-11  
 PRIOR APPLICATION NUMBER: PCT/US95/14364  
 PRIOR FILING DATE: 1995-10-25  
 PRIOR APPLICATION NUMBER: 07/332,312  
 PRIOR FILING DATE: 1994-10-31  
 NUMBER OF SEQ ID NOS: 74  
 SEQ ID NO: 60  
 LENGTH: 426  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-870-492-60

Query Match 97.8%; Score 2054; DB 17; Length 426;  
 Best Local Similarity 98.3%; Pred. No. 8e-184;  
 Matches 404; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MAAPDILDPKSAQNSKPKLPSFKPTVLAQVSEDTINTMKWKTIVSTIFLVVLYLII 60  
 Db 16 VAAPDILDPKSAQNSKPKLPSFKPTVLAQVSEDTINTMKWKTIVSTIFLVVLYLII 75

Qy 61 GATVFKALEQPKHEISORTTIVQKPFISQHSCVNSTELDELIQVVAANAGIPIGNT 120  
 Db 76 GATVFKALEQPKHEISORTTIVQKPFISQHSCVNSTELDELIQVVAANAGIPIGNT 135

Qy 121 SNOQISHWDLGSSFFAGTVTTGGGNISPTEGGKFCIYALGIPFGPLLAGVGQDQ 180  
 Db 136 SNOQISHWDLGSSFFAGTVTTGGGNISPTEGGKFCIYALGIPFGPLLAGVGQDQ 195

Query Match 98.0%; Score 2057; DB 17; Length 426;  
 Best Local Similarity 98.3%; Pred. No. 4..2e-184;

QY 181 LGTIFGKGIAKVEDTFIKNVSOTKIRIISTIIFLGCVLFVALPAIFKHIEGWSALD 240  
 Db 196 LGTIFGKGIAKVEDTFIKNVSOTKIRIISTIIFLGCVLFVALPAIFKHIEGWSALD 255

QY 241 AIFYVVTIITIGFDYVAGGSDEIYLDFXPKVWFWLVGLAYFAAVLSMIGMLRVIS 300  
 Db 256 AIFYVVTIITIGFDYVAGGSDEIYLDFXPKVWFWLVGLAYFAAVLSMIGLVRVIS 315

QY 301 KKTKEEVGEFRAAEWTANVTAEPTRRLSVEIYDFQRATSIKRKLSAELGNHQ 360  
 Db 316 KKTKEEVGEFRAAEWTANVTAEPTRRLSVEIYDFQRATSIKRKLSAELGNHQ 375

QY 361 ELTPCRRTLSVNHLTNERDVLPLKTESIYNGLTPHAGEEIAVIENTIK 411  
 Db 376 ELTPCRRTLSVNHLTNERDVLPLKTESIYNGLTPHAGEEIAVIENTIK 426

RESULT 14  
 US-10-870-492-59  
 ; Sequence 59, Application US/10870492  
 ; GENERAL INFORMATION:  
 ; APPLICANT: PAUSCH, MARK H.  
 ; TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,  
 ; FILE REFERENCE: 01142.0114 SEQUENCE LISTING  
 ; CURRENT FILING DATE: 2004-06-18  
 ; PRIOR APPLICATION NUMBER: US/10/870,492  
 ; PRIOR APPLICATION NUMBER: US/09/503, 849  
 ; PRIOR APPLICATION NUMBER: 08/816, 011  
 ; PRIOR FILING DATE: 1997-03-11  
 ; PRIOR FILING DATE: 1995-10-25  
 ; PRIOR APPLICATION NUMBER: 07/332, 312  
 ; NUMBER OF SEQ ID NOS: 74  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO: 59  
 ; LENGTH: 426  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-870-492-59

Query Match 97.8%; Score 2033; DB 17; Length 426;  
 Best Local Similarity 98.1%; Pred. No. 9 9e-184;  
 Matches 403; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVSDDTTINVMKMKTVSTIFLYVLYII 60  
 Db 16 VAADLDLDPKSAQNSKPRLSFSTKPTVLASRVSDDTTINVMKMKTVSTIFLYVLYII 75

QY 61 GATVKALEQPHETISQRTTIVIQQTFLSQHSCVNSTELLIQIVIAINAGIPLGNT 120  
 Db 76 GATVKALEQPHETISQRTTIVIQQTFLSQHSCVNSTELLIQIVIAINAGIPLGNS 120

QY 121 SNOQSHWDLGSSPFAGTIVITIGFGNISPRTEGGKIFCITYALLGTLPLGFGLAEGDQ 180  
 Db 121 SNOQSHWDLGSSPFAGTIVITIGFGNISPRTEGGKIFCITYALLGTLPLGFGLAEGDQ 180

Query Match 96.9%; Score 2035; DB 9; Length 411;  
 Best Local Similarity 95.9%; Pred. No. 4 6e-182;  
 Matches 394; Conservative 12; Mismatches 5; Indels 0; Gaps 0;

QY 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVSDDTTINVMKMKTVSTIFLYVLYII 60  
 Db 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVSDDTTINVMKMKTVSTIFLYVLYII 60

QY 61 GATVKALEQPHETISQRTTIVIQQTFLSQHSCVNSTELLIQIVIAINAGIPLGNT 120  
 Db 61 GAAVKALEQPBISQRTTIVQQTFLAQHACVNSTELLIQIVIAINAGIPLGNS 120

QY 121 SNOQSHWDLGSSPFAGTIVITIGFGNISPRTEGGKIFCITYALLGTLPLGFGLAEGDQ 180  
 Db 121 SNOQSHWDLGSSPFAGTIVITIGFGNISPRTEGGKIFCITYALLGTLPLGFGLAEGDQ 180

QY 181 LGTIFGKGIAKVEDTFIKNVSOTKIRIISTIIFLGCVLFVALPAIFKHIEGWSALD 240  
 Db 181 LGTIFGKGIAKVEDTFIKNVSOTKIRIISTIIFLGCVLFVALPAIFKHIEGWSALD 240

QY 241 AIFYVVTIITIGFDYVAGGSDEIYLDFXPKVWFWLVGLAYFAAVLSMIGDWLRVIS 300  
 Db 241 AIFYVVTIITIGFDYVAGGSDEIYLDFXPKVWFWLVGLAYFAAVLSMIGDWLRVIS 300

QY 301 KKTKEEVGEFRAAEWTANVTAEPTRRLSVEIYDFQRATSIKRKLSAELGNHQ 360  
 Db 301 KKTKEEVGEFRAAEWTANVTAEPTRRLSVEIYDFQRATSIKRKLSAELGNHQ 360

QY 361 ELTPCRRTLSVNHLTNERDVLPLKTESIYNGLTPHAGEEIAVIENTIK 411  
 Db 361 ELTPCMRTLSVNHLTSEREVPLPLKASEIYNGLTPHAGEEIAVIENTIK 411

Search completed: July 13, 2005, 09:07:00  
 Job time : 92.2442 sec8

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OM protein - protein search, using sw model

Run on: July 13, 2005, 08:10:49 ; Search time 26.3635 Seconds  
(without alignment)

1163.760 Million cell updates/sec

Title: US-09-503-089A-2  
Perfect score: 2100  
Sequence: 1 MAAPDLDPKSAQNSKPRL.....LNGLTPHCAAGEEIAVIENTK 411

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMBO.DEP:/\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMBO.DEP:/\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMBO.DEP:/\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMBO.DEP:/\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMBO.DEP:/\*  
6: /cgn2\_6/ptodata/1/iaa/backfile1..dep:/\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2095	99.8	411	3	US-09-234-080-2
2	2095	99.8	411	3	US-09-336-643A-83
3	96.9	411	3	US-09-234-080-6	
4	1824	86.9	370	3	US-09-144-914-8
5	1243	59.2	538	4	US-09-94-016-7001
6	1243	59.2	558	4	US-09-94-016-7368
7	803	38.2	393	4	US-09-435-470-2
8	803	38.2	393	4	US-09-43-470-4
9	803	38.2	419	4	US-09-616-6913
10	803	38.2	440	4	US-09-94-016-7809
11	547	26.0	107	3	US-09-234-080-4
12	427	20.3	499	4	US-09-56-763-2
13	427	20.3	499	4	US-09-431-367B-2
14	391	18.6	332	4	US-09-56-763-5
15	391	18.6	332	4	US-09-431-367B-5
16	382	18.2	361	4	US-09-365-842-14
17	379.5	18.1	336	3	US-08-74-816-2
18	379.5	18.1	336	3	US-09-144-914-2
19	363	17.3	394	3	US-09-144-914-4
20	349.5	16.6	388	4	US-09-94-016-7631
21	348	16.6	313	4	US-09-336-643A-81
22	348	16.6	313	4	US-09-56-763-8
23	348	16.6	313	4	US-09-431-367B-8
24	337	16.0	405	3	US-09-144-914-5
25	309.5	14.7	408	4	US-09-365-842-12
26	291.5	13.9	618	1	US-08-33-312-2
27	284	13.5	257	4	US-09-94-016-6654

## ALIGNMENTS

RESULT 1  
US-09-336-080-2  
; Sequence 2, Application US/09236080  
; Patent No. 6242217  
; GENERAL INFORMATION:  
; APPLICANT: Helen Meadowbs  
; FILE REFERENCE: GB30031  
; CURRENT APPLICATION NUMBER: US/09-236,080  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO: 2  
; LENGTH: 411  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-236-080-2

Query Match 99.8%; Score 2095; DB 3; Length 411;  
Best Local Similarity 99.8%; Pred. No. 4.7e-205;  
Matches 410; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	1 MAAPDLDPKSAQNSKPRLSFKPTVLSRVS E DTTINYMKWKT VSTI F L V Y L I I 60
Db	1 MAAPDLDPKSAQNSKPRLSFKPTVLSRVS E DTTINYMKWKT VSTI F L V Y L I I 60
Qy	61 GATVYKALEQPHESIORTTIVIQKOPFISQCNVNSTELDIQI QVVA INAGI I P G N T 120
Db	61 GATVYKALEQPHESIORTTIVIQKOPFISQCNVNSTELDIQI QVVA INAGI I P G N T 120
Qy	121 SNOISHDLGSSFFFGATVITIGFGNISPRTEGGKFCITYALGIPFLFGFLAGYGDQ 180
Db	121 SNOISHDLGSSFFFGATVITIGFGNISPRTEGGKFCITYALGIPFLFGFLAGYGDQ 180
Qy	181 LGTFGKGIAKVE DTFIKWVNSQTKIRIISTIIFLGCVLFV ALPA T I K H E G W S A D 240
Db	181 LGTFGKGIAKVE DTFIKWVNSQTKIRIISTIIFLGCVLFV ALPA T I K H E G W S A D 240
Qy	241 AIVFWVITLTIGFGDYVAGSDIEYLDFYKPWVWFLVGLAYFAVLSMIGDWLRVIS 300
Db	241 AIVFWVITLTIGFGDYVAGSDIEYLDFYKPWVWFLVGLAYFAVLSMIGDWLRVIS 300
Qy	301 KCTKEEVEFRAHA E NT A E F K T R R I S V E Y D K F O R A T S I K R L S A B L G H N Q 360
Db	301 KCTKEEVEFRAHA E NT A E F K T R R I S V E Y D K F O R A T S I K R L S A B L G H N Q 360

RESULT 2  
US-09-336-633A-83  
Sequence 83, Application US/09336643A  
Patent No. 6398761  
GENERAL INFORMATION  
APPLICANT: Miller, Andrew P.  
CURR. APPLICANT: Curran, Mark Edward  
APPLICANT: Hu, Ping  
APPLICANT: Rutter, Marc  
TITLE OF INVENTION: No. 6399161el Human Potassium Channels  
CURRENT APPLICATION NUMBER: US/09/336,643A  
CURRENT FILING DATE: 1999-06-18  
PRIOR FILING DATE: 1998-08-07  
PRIOR APPLICATION NUMBER: 60/076,687  
PRIOR APPLICATION NUMBER: 60/116,448  
PRIOR FILING DATE: 1999-01-19  
PRIOR FILING DATE: 1999-02-22  
NUMBER OF SEQ ID NOS: 87  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO: 83  
TYPE: PRT  
ORGANISM: H. sapiens  
US-09-336-633A-83

Query Match 99.8%; Score 2095; DB 3; Length 411;  
Best Local Similarity 99.8%; Pred. No. 4.7e-205; Indels 0; Gaps 0;  
Matches 410; Conservative 1; Mismatches 0; Delins 0; Gaps 0;

Qy 1 MAAPDLDPKSAAQNSKPRLSSTKPTVLASRVESTDINMKWKTSTFLVVVLYLI 60  
Db 1 MAAPDLDPKSAAQNSKPRLSSTKPTVLASRVESTDINMKWKTSTFLVVVLYLI 60

Qy 61 GATVFKALEQPHESQRTTIVQKOTFISOHSCVNSTELDELIOQIVAAINAGIPLGNT 120  
Db 61 GATVFKALEQPHESQRTTIVQKOTFISOHSCVNSTELDELIOQIVAAINAGIPLGNT 120

Qy 121 SNOISHMDLGSSFFAGTVTTIGFGENISPRTEGGKIFCIIYALGIPFGLLAGVGDQ 180  
Db 121 SNOISHMDLGSSFFAGTVTTIGFGENISPRTEGGKIFCIIYALGIPFGLLAGVGDQ 180

Qy 181 LGTIFGKGIAKVEDTFIKWNSQTKRIISTIIFLFGCVLFVALPAIFHIGMSALD 240  
Db 181 LGTIFGKGIAKVEDTFIKWNSQTKRIISTIIFLFGCVLFVALPAIFHIGMSALD 240

Qy 241 AIYFVVTITLTIGFGDYVAGGSDEIYLDFYKPVVVFILVGLAYFAAVLSMIGDWLRVIS 300  
Db 241 AIYFVVTITLTIGFGDYVAGGSDEIYLDFYKPVVVFILVGLAYFAAVLSMIGDWLRVIS 300

Qy 301 KKTKEEVGEFRAAETNTAAEKFTRRLSVEIYDKFORATSKRKLSAELAGHNQ 360  
Db 301 KKTKEEVGEFRAAETNTAAEKFTRRLSVEIYDKFORATSKRKLSAELAGHNQ 360

Qy 361 ELTPCRTLSVNLINERDVLPPLKTESIYLNGLTPHAGEBEIAVENIK 411  
Db 361 ELTPCRTLSVNLINERDVLPPLKTESIYLNGLTPHAGEBEIAVENIK 411

RESULT 4  
US-09-144-914-8  
Sequence 8, Application US/09144914  
Patent No. 63109855  
GENERAL INFORMATION:  
APPLICANT: Duprat, Fabrice  
APPLICANT: Le sage, Florian  
APPLICANT: Pinc, Michel  
APPLICANT: Lazdunski, Michel  
TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS  
FILE REFERENCE: 989.6705CIP  
CURRENT APPLICATION NUMBER: US/09/144,914  
CURRENT FILING DATE: 1996-09-01  
EARLIER APPLICATION NUMBER: US/09/144,914  
EARLIER FILING DATE: 1996-11-15  
EARLIER APPLICATION NUMBER: 60/095,234  
EARLIER FILING DATE: 1998-08-04  
EARLIER APPLICATION NUMBER: FR 96/01565  
EARLIER FILING DATE: 1996-02-08  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO: 8  
LENGTH: 370  
TYPE: PRT  
ORGANISM: Murine  
FEATURE:  
OTHER INFORMATION: TREK-1  
US-09-144-914-8

Query Match 86.9%; Score 1824; DB 3; Length 370;

Best Local Similarity 96.5%; Pred. No. 1.8e-177; Matches 355; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MAPDLDPKSAQNSKPRLSFSTKPTVLASRVEDDTINVMKKTIVSTIFLVVLYLII 60 Db 1 MAPDLDPKSAQNSKPRLSFSTKPTVLASRVEDDTINVMKKTIVSTIFLVVLYLII 60

Qy 61 GATVFKALEQPHBISQRTTIVKOTFISQHSCVNSTEDELIOQIVAAINAGIPLGNT 120 Db 61 GAAVKALEQPOESQRITIVKOTFIAQHACTVNSTEDELIOQIVAAINAGIPLGNS 120

Qy 121 SNOISHWDLGSSPFAGTTGIFTTGFGNISPRTEGGKIFCITYALLGIPFLFGVGDQ 180 Db 121 SNOVSHWLGSSEFFAGTTGIFTTGFGNISPRTEGGKIFCITYALLGIPFLFGVGDQ 180

Qy 181 LGTIFRGKIAKVEDETFIKWNVSKTKIRILISTIPILEGCVLFLVALPALEKHKIEGWSALD 240 Db 181 LGTIFRGKIAKVEDETFIKWNVSKTKIRILISTIPILEGCVLFLVALPALEKHKIEGWSALD 240

Qy 241 AIFYVVTLLTIGFDDYAGGSDEIYDFYKPVWFWLVLGLAYFAAVLSMGDLRLVIS 300 Db 241 AIFYVVTLLTIGFDDYAGGSDEIYDFYKPVWFWLVLGLAYFAAVLSMGDLRLVIS 300

Qy 301 KCTKEEKEYGEFRAAAENTANVTAEFKETRRLSVEIYDKFORATSIKRKSLAELAGHQ 360 Db 301 KCTKEEVEFRAAAENTANVTAEFKETRRLSVEIYDKFORATSIKRKSLAELAGHQ 360

Qy 361 EITPCRTT 368 Db 361 EITPCMRT 368

RESULT 5 US-09-949-016-7001 ; Sequence 7001, Application US/09949016 ; GENERAL INFORMATION: ; PATENT NO. 6812339 ; APPLICANT: VENTER, J. Craig et al. ; TITLE OF INVENTION: KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF ; FILE REFERENCE: CL001307

Qy CURRENT APPLICATION NUMBER: US/09/949, 016 ; CURRENT FILING DATE: 2000-04-14 ; PRIOR APPLICATION NUMBER: 60/241,755 ; PRIOR FILING DATE: 2000-10-20 ; PRIOR APPLICATION NUMBER: 60/237,768 ; PRIOR FILING DATE: 2000-10-03 ; PRIOR APPLICATION NUMBER: 60/231,498 ; NUMBER OF SEQ ID NOS: 207012 ; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO: 73-8

Qy 2 AAPDUDPKSA-----AONSKPLRSFSTKPTVLASRVEDT--TINYMKWKTSTI 50 Db 37 AAAPVCOPKSATNGOPPAPAPTPTPLSISRAVVAA-RMETSQGGIOTWKWKTVAI 95

Qy 51 FLYVWVYLIGATVEKALEQPHEISORTTIVQKOTFISQHSCVNSTEDLIQIVVAAI 110 Db 96 FVWVWVYLVTGCLVRALEQFESSIONTIALEKAFLRDVCPSPOLETLJQHADAD 155

Qy 111 NAGIIPLGNTSNQI SHWDLGSSPFAGTTGIFTTGFGNISPRTEGGKIFCITYALLGIPFL 170 Db 156 NAGVSPIGNSNNNHHWDLGSSPFAGTTGIFTTGFGNISPRTEGGKIFCITYALLGIPFL 215

Qy CURRENT APPLICATION NUMBER: US/09/949, 016 ; CURRENT FILING DATE: 2000-04-14 ; PRIOR APPLICATION NUMBER: 60/241,755 ; PRIOR FILING DATE: 2000-10-20 ; PRIOR APPLICATION NUMBER: 60/237,768 ; PRIOR FILING DATE: 2000-10-03 ; PRIOR APPLICATION NUMBER: 60/231,498 ; PRIOR FILING DATE: 2000-09-08 ; NUMBER OF SEQ ID NOS: 207012 ; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO: 7001 ; LENGTH: 538 ; TYPE: PRT ; ORGANISM: Human ; US-09-949-016-7001

Qy 2 AAPDUDPKSA-----AONSKPLRSFSTKPTVLASRVEDT--TINYMKWKTSTI 50 Db 17 AAAPVCOPKSATNGOPPAPAPTPTPLSISRAVVAA-RMETSQGGIOTWKWKTVAI 75

Qy 51 FLYVWVYLIGATVEKALEQPHEISORTTIVQKOTFISQHSCVNSTEDLIQIVVAAI 110 Db 76 FVWVWVYLVTGCLVRALEQFESSIONTIALEKAFLRDVCPSPOLETLJQHADAD 135

Qy 111 NAGIIPLGNTSNQI SHWDLGSSPFAGTTGIFTTGFGNISPRTEGGKIFCITYALLGIPFL 170 Db 136 NAGVSPIGNSNNNHHWDLGSSPFAGTTGIFTTGFGNISPRTEGGKIFCILIAFGIPFL 195

Qy CURRENT APPLICATION NUMBER: US/09/949, 016 ; CURRENT FILING DATE: 2000-04-14 ; PRIOR APPLICATION NUMBER: 60/241,755 ; PRIOR FILING DATE: 2000-10-20 ; PRIOR APPLICATION NUMBER: 60/237,768 ; PRIOR FILING DATE: 2000-10-03 ; PRIOR APPLICATION NUMBER: 60/231,498 ; NUMBER OF SEQ ID NOS: 207012 ; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO: 73-8

Qy 171 GFLIAGVGDDQDGTGKGAKVEDTICKWNVSKTKIRILISTIPILEGCVLFLVALPALEKHKIEGWSALD 240 Db 216 GFLIAGVGDDQDGTGKGAKVEDTICKWNVSKTKIRILISTIPILEGCVLFLVALPALEKHKIEGWSALD 240

Qy 231 KHEGMALSALDAYFVWTLLTIGFDDYAGGSDEIYDFYKPVWFWLVLGLAYFAAVL 289 Db 276 KYIEWTGALESIYFVWTLLTIGFDDYAGGSDEIYDFYKPVWFWLVLGLAYFAAVL 335

Qy 290 SMIGDWLRLVSKTKTEEVGEFRAAAENTANVTAEFKETRRLSVEIYDKFORATSIKRK 349 Db 336 SMIGDWLRLVSKTKTEEVGEFRAAAENTANVTAEFKETRRLSVEIHDKLQRAATIR-- 393

Qy 350 LSAELAGNHNNOBLTPERTLSVNHLTNERDVLP 383 Db 374 -SME-----RRRUGLDQAHSDLMLSP 394

Qy 171 GFLIAGVGDDQDGTGKGAKVEDTICKWNVSKTKIRILISTIPILEGCVLFLVALPALEKHKIEGWSALD 240 Db 216 GFLIAGVGDDQDGTGKGAKVEDTICKWNVSKTKIRILISTIPILEGCVLFLVALPALEKHKIEGWSALD 240

Qy 231 KHEGMALSALDAYFVWTLLTIGFDDYAGGSDEIYDFYKPVWFWLVLGLAYFAAVL 289 Db 276 KYIEWTGALESIYFVWTLLTIGFDDYAGGSDEIYDFYKPVWFWLVLGLAYFAAVL 335

Qy 290 SMIGDWLRLVSKTKTEEVGEFRAAAENTANVTAEFKETRRLSVEIYDKFORATSIKRK 349 Db 336 SMIGDWLRLVSKTKTEEVGEFRAAAENTANVTAEFKETRRLSVEIHDKLQRAATIR-- 393

Qy 350 LSAELAGNHNNOBLTPERTLSVNHLTNERDVLP 383 Db 374 -SME-----RRRUGLDQAHSDLMLSP 394

**RESULT 7** US-09-432-470-2 Application US/09432470

Sequence 4, Application US/09432470

GENERAL INFORMATION:

APPLICANT: David Malcolm Duckworth

TITLE OF INVENTION: NOVEL COMPOUNDS

FILE REFERENCE: GP-30190

CURRENT APPLICATION NUMBER: US/09/432,470

CURRENT FILING DATE: 1999-11-03

EARLIER APPLICATION NUMBER: UK 9923668.9

EARLIER FILING DATE: 1999-10-07

EARLIER APPLICATION NUMBER: UK 9824048.4

EARLIER FILING DATE: 1998-11-03

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 2

TYPE: PRT

ORGANISM: HOMO SAPIENS

US-09-432-470-2

Query Match Score 38.2%; Best Local Similarity 51.1%; Pred. No. 3e-73; Length 393; Matches 145; Conservative 61; Mismatches 76; Indels 2; Gaps 1;

Qy 42 MKWKTVSTIPLLVLIGATVFKALEQPHESORTTIVIQKOTFISQHSCVNTELDE 101  
Db 1 MRSTTLALLAALVLVSGALVFRALQEPRQQARELGEVREKFLRAHCVSDQBLGL 60

Qy 102 LIQQIVAAINAGIPLGNTSNQISH - WDLGSSFFAGTVITIGGNISPRTEGGKIFC 159  
Db 61 LIKEVADALGGADPETNSTNSNSHSSAWDLGSAFFSGTIIITIGVNVALRTDGRFLFC 120

Qy 160 IYALLGIPLFGLLAGVGDQGTIFGKGIAKVEDTPIKVNQSQTKIRIISTIFLLFGC 219  
Db 121 IFYALVGPALIIFKHIEGMSALDAIYFVYTTLTIGFDYVAGGSDEIYLDFYKPVWFWIL 279

Qy 220 VLFWVALPAIIFKHIEGMSALDAIYFVYTTLTIGFDYVAGGSDEIYLDFYKPVWFWIL 279  
Db 181 LLFVLVTPFVFCYMEDNSKLEAIFTVLTIGFDYVAGADPROSPAYQPLVNFWIL 240

Qy 280 VGLAYFAAVLSMIGDWLRVISKKTKEEVGEFRAHAETANTVA 323  
Db 241 LGLAYFAASVLTIGNWLRVVSRRTAEMGGLTAAQASWTGTVTA 284

RESULT 8 US-09-432-470-4 Application US/09432470

Sequence 4, Application US/09432470

GENERAL INFORMATION:

APPLICANT: David Malcolm Duckworth

TITLE OF INVENTION: NOVEL COMPOUNDS

FILE REFERENCE: GP-30190

CURRENT APPLICATION NUMBER: US/09/432,470

CURRENT FILING DATE: 1999-11-03

EARLIER APPLICATION NUMBER: UK 9923668.9

EARLIER FILING DATE: 1999-10-07

EARLIER APPLICATION NUMBER: UK 9824048.4

EARLIER FILING DATE: 1998-11-03

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 4

TYPE: PRT

ORGANISM: HOMO SAPIENS

US-09-432-470-4

Query Match Score 38.2%; Best Local Similarity 51.1%; Pred. No. 3.3e-73; Length 419; Matches 145; Conservative 61; Mismatches 76; Indels 2; Gaps 1;

Qy 42 MKWKTVSTIPLLVLIGATVFKALEQPHESORTTIVIQKOTFISQHSCVNTELDE 101  
Db 27 MRSTTLALLAALVLVSGALVFRALQEPRQQARELGEVREKFLRAHCVSDQBLGL 86

Qy 102 LIQQIVAAINAGIPLGNTSNQISH - WDLGSSFFAGTVITIGGNISPRTEGGKIFC 159  
Db 87 LIKEVADALGGADPETNSTNSNSHSSAWDLGSAFFSGTIIITIGVNVALRTDGRFLFC 146

Qy 160 IYALLGIPLFGLLAGVGDQGTIFGKGIAKVEDTPIKVNQSQTKIRIISTIFLLFGC 219  
Db 147 IFYALVGPALIIFKHIEGMSALDAIYFVYTTLTIGFDYVAGGSDEIYLDFYKPVWFWIL 279

Qy 220 VLFWVALPAIIFKHIEGMSALDAIYFVYTTLTIGFDYVAGGSDEIYLDFYKPVWFWIL 279  
Db 207 LLFVLVTPFVFCYMEDNSKLEAIFTVLTIGFDYVAGADPROSPAYQPLVNFWIL 266

Qy 280 VGLAYFAAVLSMIGDWLRVISKKTKEEVGEFRAHAETANTVA 323  
Db 267 LGLAYFAASVLTIGNWLRVVSRRTAEMGGLTAAQASWTGTVTA 310

RESULT 10  
 US-09-949-016-7809  
 Sequence 7609, Application US/09949016  
 Patent No. 6812339  
 GENERAL INFORMATION:  
 APPLICANT: VENTER, J. Craig et al.  
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 FILE REFERENCE: CLO001307  
 CURRENT APPLICATION NUMBER: US/09/949, 016  
 CURRENT FILING DATE: 2000-04-14  
 PRIOR APPLICATION NUMBER: 60/241,755  
 PRIOR FILING DATE: 2000-10-20  
 PRIOR FILING DATE: 2000-10-03  
 PRIOR APPLICATION NUMBER: 60/231,498  
 PRIOR FILING DATE: 2000-09-08  
 NUMBER OF SEQ ID NOS: 207012  
 SOFTWARE: FASTSEQ for Windows Version 4.0  
 SEQ ID NO: 7809  
 LENGTH: 440  
 TYPE: PRT  
 ORGANISM: Human  
 US-09-249-016-7809

Query Match 38.2%; Score 803; DB 4; Length 440;  
 Best Local Similarity 51.1%; Pred. No. 3 5e-73;  
 Matches 145; Conservative 61; Mismatches 76; Indels 2; Gaps 1;

Qy 42 MKWKTIVSTIFLVVYLIGATYVKALSOPEHISQRTTIVIQKOTFISQHSCVNSTELDE 101  
 Db 48 MRSTILLALLVYLISGALVERAEPHEOAQRIGEVREKFRLAHPCVSDQELGL 107  
 Qy 102 LIQIVAAINAGIPLGNTSNQISH- -WDLGSSPFPAQTIVITIGFNISPRTEGGKTPC 159  
 Db 108 LTKEVADLGGADPETSNSHSANLDGSAFFSTTITIGYNVALRTDAGRFLC 167  
 Qy 160 ITYALLGPFLPGFLLAGTGDQLETFIKWVTSQTKRIRISTTIFLFGC 219  
 Db 168 IFYALVGVLPGFLLAGTGDQLESLRQGIGHTEAIFPKWAVPPELVRLSAMFLLGC 227  
 Qy 220 VLFVALPAFKHTEGWSALDAITYFVVTLTGFDYVAGGSDFIEYDFKPVVWFWIL 279  
 Db 228 LLPVLPVTPFVFCYMEDWSLKEATYFVVTLTGFDYVAGADPQSPAYPLVWFWIL 287  
 Qy 280 VGLAYFAAVLTSMIGDMLRIVSKTKEEYGEFRHAETTANTAA 323  
 Db 288 LGLAYFAVSLTTGNWLRVSRTRRAENGGLTQAASWTGTVA 331

RESULT 11  
 US-09-236-080-4  
 Sequence 4, Application US/09236080  
 Patent No. 6242217  
 GENERAL INFORMATION:  
 APPLICANT: Helen Meadows  
 APPLICANT: Conrad Chapman  
 TITLE OF INVENTION: No. 6242217e1 Compounds  
 CURRENT APPLICATION NUMBER: US/09/236, 080  
 CURRENT FILING DATE: 1999-01-25  
 NUMBER OF SEQ ID NOS: 6  
 SOFTWARE: Fast-SEQ for Windows Version 3.0  
 SEQ ID NO 4  
 LENGTH: 107  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-236-080-4

Query Match 26.0%; Score 547; DB 3; Length 107;  
 Best Local Similarity 98.1%; Pred. No. 5.6e-46;

RESULT 12  
 US-09-561-763-2  
 Sequence 2, Application US/09561763  
 Patent No. 666373  
 GENERAL INFORMATION:  
 APPLICANT: Curtis, Rory A.J. et al.  
 TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR  
 FILE REFERENCE: MN1-074CP2  
 CURRENT APPLICATION NUMBER: US/09/561,763  
 CURRENT FILING DATE: 2000-04-29  
 PRIOR APPLICATION NUMBER: 09/431,367  
 PRIOR FILING DATE: 01-11-1999  
 PRIOR APPLICATION NUMBER: US 09/259,851  
 PRIOR FILING DATE: 01-03-1999  
 NUMBER OF SEQ ID NOS: 12  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 2  
 LENGTH: 499  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-561-763-2

Query Match 20.3%; Score 427; DB 4; Length 499;  
 Best Local Similarity 31.1%; Pred. No. 1e-34;  
 Matches 106; Conservative 60; Mismatches 121; Indels 54; Gaps 11;

Qy 54 VVLYLIGATYVKALEQPHEISQRTTIVQKOTFISQHSCVNSTELDELIQQVAAINAG 113  
 Db 12 IIYLYTAAGAAIPFVELEEEHWEKAAKNYYTOKHLKEFPCLQGEGLDKILEVSDAACQ 71  
 Qy 114 IIPLGNTSNQISHWLGSFFPATGTVTTIGFNISPRTEGGKFCITYALGIPFLGPL 173  
 Db 72 VAITGNQT- -FNNWNWNAIMAPATVTTIGVNVAKPTPAGRLFCVYGLRGVPL--C 126  
 Qy 174 LACVGDOIQTGTTKGKIAKVEDFTKVNVSOTKIRIRISTTIFLFGCVLFLVALPAIIPH 233  
 Db 127 LTW-SAUGKFFGAKRLQGQLTRKRSLSRKQITCIVIIVGVVLHVIPIPFPVFRVT 185  
 Qy 234 EGWSALDAIYFVVTLTGFDYVAG-GSD1EYLDLDEYKPVVWFWILVGLAYPAVLSMI 292  
 Db 186 EGNYIYGLYSFTISTIGRSDFVAGVNPNSANYHALYRYFVELWYIGLAW--LSLF 241  
 Qy 293 GDMLRVLISKTKYKEEVGFSRHAETWTAFFKETRRLSVTVEYDQFQRTASIKRKLSA 352  
 Db 242 VNM-----KVSMF-----VEVHKAIKKRR-----RKESF 267

RESULT 13  
 US-09-431-367B-2  
 Sequence 2, Application US/09431367B  
 Patent No. 6670149  
 GENERAL INFORMATION:  
 APPLICANT: Curtis, Rory A.J.  
 TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR  
 FILE REFERENCE: MN1-074CP  
 CURRENT APPLICATION NUMBER: US/09/431,367B  
 CURRENT FILING DATE: 1999-11-01  
 PRIOR APPLICATION NUMBER: 09/259,951

PRIOR FILING DATE:	1999-03-01
NUMBER OF SEQ ID NOS:	12
SOFTWARE:	PatentIn Ver. 2.0
SEQ ID NO:	2
LENGTH:	499
TYPE:	PRT
ORGANISM:	Homo sapiens
US-09-431-367B-2	
Query Match	20.3%; Score 427; DB 4; Length 499;
Best Local Similarity	31.1%; Pred. No. 1e-34;
Matches	106; Conservative 60; Mismatches 121; Indels 54; Gaps 11;
Db	54 VVLLIGATVKALEQPHEISQRTTIVIQKQTFTSQHSVCVNSTELDELQIQIVAAING 113 12 IIFYAIGAIAKFEVLEEPWKEAKENYNTOKLHLKEFPLDKEVSDAACG 71
Qy	114 IILPGLTSNQISHWDLGSSPFPAAGTVITITGGFQNSPRTEGGKAFCLIALLGPFGLI 173 72 VAITGNOT--FNNNNWPNAPIFAATVITIGYGNVAPKTPAGRFLCFCVFGYGPL--C 126
Db	174 LAGVGDQLGTIFGKGIAKAVDTFIKWNVSQWKIRIISTTIFLCVCLFVALPATIKHI 233 127 LTWI-SNALGPGFFGGRKRLGFLTRGVSKRAQITCTVTFIVCVLWVIPPFVEMT 185
Qy	234 EGWSALDAIYFVVITLTGFDYAG-GSDIEYLDFYKEVVFNLVCGAYFAAVLSMI 292 186 EGWNGLGGLYSFITSITGFDFYAGVNPNSANTHALYRFVEMIYGLGAW---LSLF 241
Db	293 GDWLKVISKTKTKEVGRHAAETWANTAEKFTRRISVELYDKFQRATSIKRKLSA 352 242 VNW-----KVSME-----VEVHAIKERRR-----RKESF 267
Qy	353 ELAGHNHQELTPCRRTLSVNHLTNERDV--LPPLKRTTESTY 391 268 E-SSPHS-----RKALQVKGSTASRDVNIFSFLSKREETY 301
Db	
RESULT 14	
US-09-561-763-5	Sequence 5, Application US/09561763
Db	; General Information: SEQ ID NO: 6664373 ; General Information: CURTIS, RORY A. J. et al. ; Applicant: CURTIS, RORY A. J. et al. ; Title of Invention: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR ; File Reference: MNI-074CP2 ; Current Application Number: US/09/561,763 ; Current Filing Date: 2000-04-29 ; Prior Application Number: 09/431,367 ; Prior Filing Date: 01-11-1999 ; Prior Application Number: US 09/259,951 ; Prior Filing Date: 01-03-1999 ; Number of SEQ ID NOS: 12 ; Software: PatentIn Ver. 2.0 ; SEQ ID NO: 5 ; LENGTH: 332
Qy	Query Match 18.6%; Score 391; DB 4; Length 332;
Best Local Similarity	35.9%; Pred. No. 2.5e-31;
Matches	89; Conservative 51; Mismatches 94; Indels 14; Gaps 6;
Db	50 IFLVVVLYLIGATVKALEQPHEISQRTTIVIQKQTFTSQHSVCVNSTELDELQIQVA 109 25 LLLAYAYLAIGTGVWTLERGAQDSSRSFQRDPALDSLRDVQA 84
Qy	110 INAGITPLGNTSNQISHWDLGSSPFPAAGTVITITGGFQNSPRTEGGKIFCLIALLGIP 143 170 FGFLLAGVGDOLGTIFGKG3I---AKVETDTFIKWNVSQPKIRIISTTIFLGCTLVFVAL 225
Db	144 NLVVL---NRLGHMMQQVNHWAISRLGGT---WQ-DPDKARWLGSALLSGLFLLL 195
Qy	226 PAILPKHIEGMSALAAIYFVVITLTGFDYAGGSDIE YLDDEYKPVVWFVILVGLAY 284 196 PPLFSHMEGWSYTFGYFAFITLSTVGFDYVGMNPSQRYPWYKCNMVSLSLWIFGMAW 255
Db	
Qy	285 FAAVLSMI 292 256 LALIKLI 263
Db	
Search completed: July 13, 2005, 08:47:04	
Job time :	28.3635 secs